

1 10 20 30 40 50 60 70 80 90 100  
 |-----|-----|-----|-----|-----|  
 human MRPQGPAAAPQRLRGL--LLLLLLQLPAPSSASEIPKQKQKQALRQREVVDLYNGMCLQGPAGVPGROGSPGANGIPGTPGIPGRDGFKEGKECLRESF  
 mouse MRPQGRAAPPQLLGLFLVLLLLQLSAPSSASENPKVKQKALIRQREVVDLYNGMCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGFKEGKECLRESF  
 rice\_fish MTPLSPRLLIILCLALPLHGQE--KGRSRGVRKDPDADKF--GSCLOGPAGTPGRDGNPANGIPGTPGIPGRDGLKGEKGEVCVSEVF  
 zebra\_fish MGTKLTLQLLICFWISLPFCVTQKAKERIPRQ--RDAEFTDKYQA--CVQGVPGVQGRDGNPANGIPGTPGIPGRDGLKGEKGEVCVSEVF  
 chicken RPREVLEAYNGVCLQGPSGVPGRDGNPANGIPGTPGIPGRDGPKEGKECLRESI  
 Consensus .....ll.....p.....k.....r.r#v...yng.ClQGp.GvpGRDGNpG.NGIPGTPGIPGRDG.KGEKGECLresf  
 101 110 120 130 140 150 160 170 180 190 200  
 |-----|-----|-----|-----|-----|  
 human EESWTPNYKQCSWSSSLNYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRYWYFTFNGAECSGPLPIEAIYYLDQGSPEMNSTINIHRTSSVE  
 mouse EESWTPNYKQCSWSSSLNYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRYWYFTFNGAECSGPLPIEAIYYLDQGSPELNSTINIHRTSSVE  
 rice\_fish EEPWKPNYKQCAWNSLNYGIDLGKIAECTFTKLRSALRVLFTGSLRLKCKEACCQRYWYFTFDGAECTGPLPVESIIYLNQGSPELNSTINIHRTSSVE  
 zebra\_fish EEPWKPNFKQCAWNSLNYGIDLGKIAECTFTKQSDSALRVLFSGSLRLKCKTACCQRYWYFTFNGAECTGPLPIESIVYLDQGSPELNSTINIHRTSTVE  
 chicken EESWTPNFKQCSWNSALNYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRSACCQRYWYFTFNGAECAGPLPIEAIYYLDQGSPELNSTINIHRTSSVE  
 Consensus EESwtPN%KQCSwssLNYGIDLGKIA#CTFTKnrS#SALRVLFSGSLRLKCr.ACCQRYWYFTF#GAEC.GPLP!Eai!YL#QGSPE\$NSTINIHRTSSVE

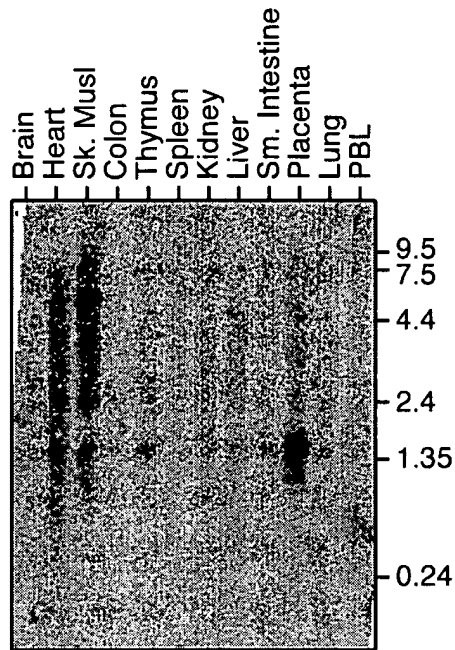
FIG. 1

201 210 220 230 240 245  
 |-----|-----|-----|-----|  
 human GLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNVSRSRIIEELPK  
 mouse GLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNVSRSRIIEELPK  
 rice\_fish GLCEGIGAGLVDVALWVGTCADYPRGDASTGWNVSRSRIIEELPK  
 zebra\_fish GLCEGIHAGLVDVGIWVGTCADYPRGDASTGWNVSRSRIIEELPK  
 chicken GLCEGINAGLVDIAIWVGTCSDYPRGDASTGWNVSRSRIIEELPK  
 Consensus GLCEGI.AGLVD!aiWVGTCsDYPrgDASTGWNVSRSRIIEELPK

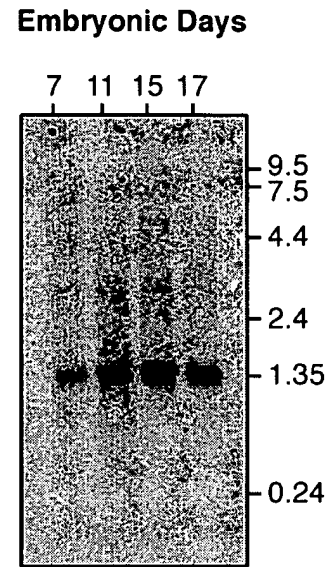
10 20 30 40 50  
 |-----|-----|-----|-----|  
 MRPQGPAAAPQRLRGLLLLLLLQLPAPSSASEIPKQKQKQALRQREVVDLYNG  
 60 70 80 90 100  
 |-----|-----|-----|-----|  
 MCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGFKEGKECLRESFEESWTPNY  
 110 120 130 140 150  
 |-----|-----|-----|-----|  
 KQCSWSSSLNYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRYWYF  
 160 170 180 190 200 210  
 |-----|-----|-----|-----|  
 TFNGAECSGPLPIEAIYYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVA  
 220 230 240  
 |-----|-----|  
 IWVGTCSDYPRGDASTGWNVSRSRIIEELPK

FIG. 2

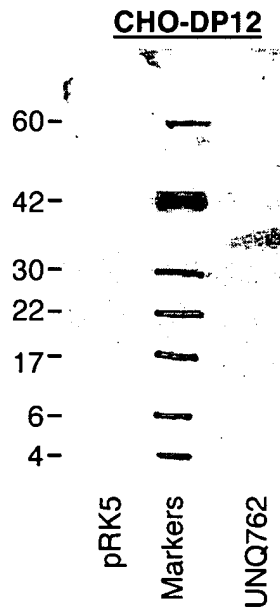
2 / 74



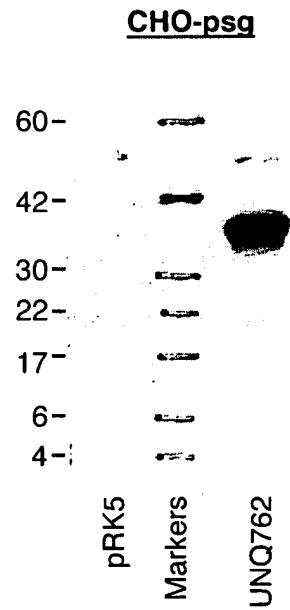
**FIG. 3A**



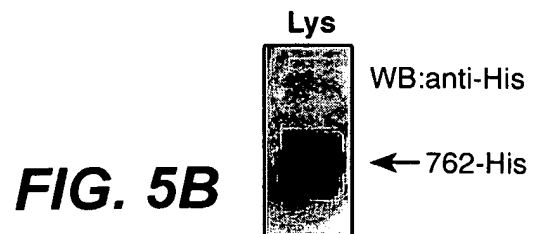
**FIG. 3B**



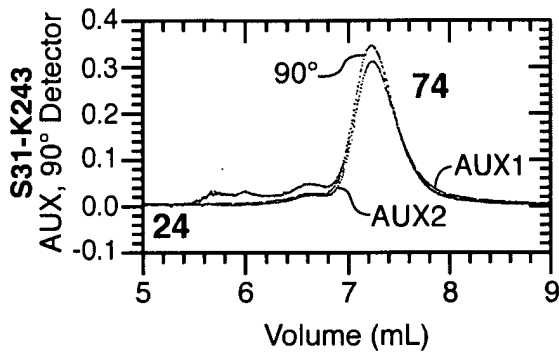
**FIG. 4A**



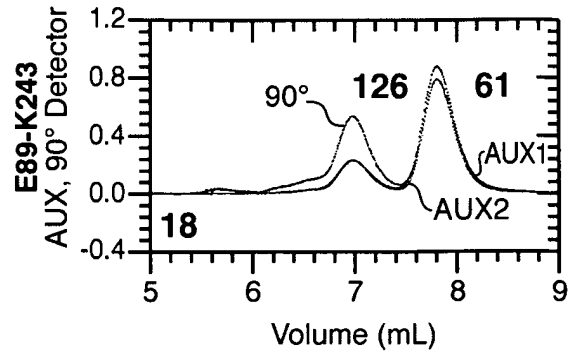
**FIG. 4B**



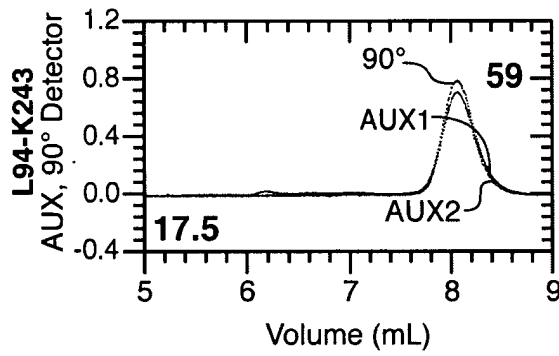
3 / 74



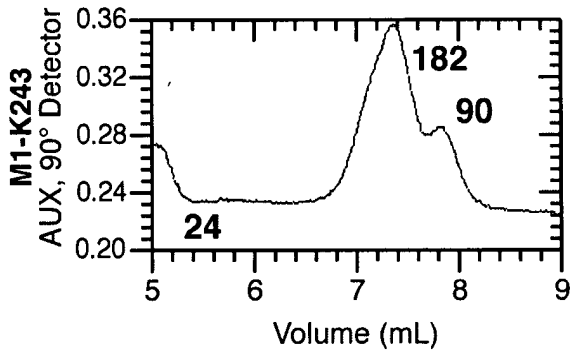
**FIG. 6A**



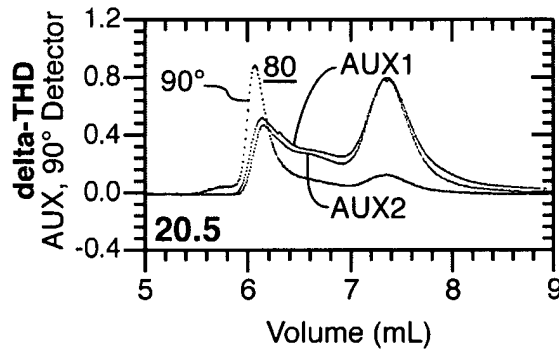
**FIG. 6B**



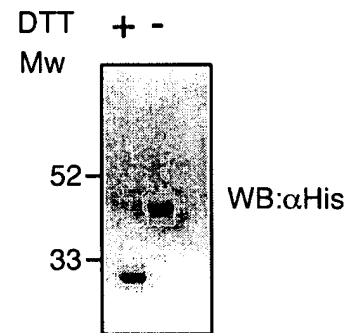
**FIG. 6C**



**FIG. 7A**

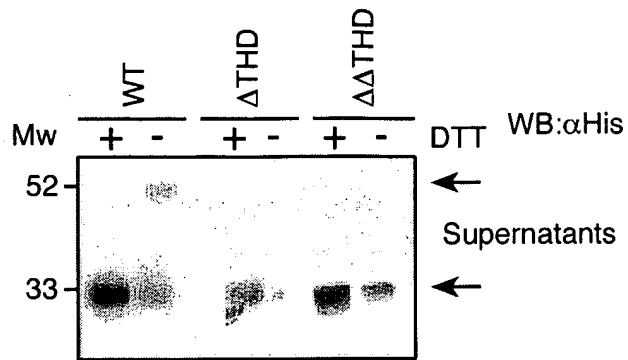


**FIG. 7B**

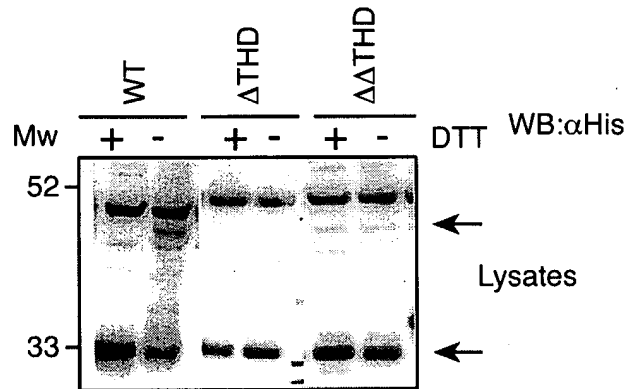


**FIG. 7C**

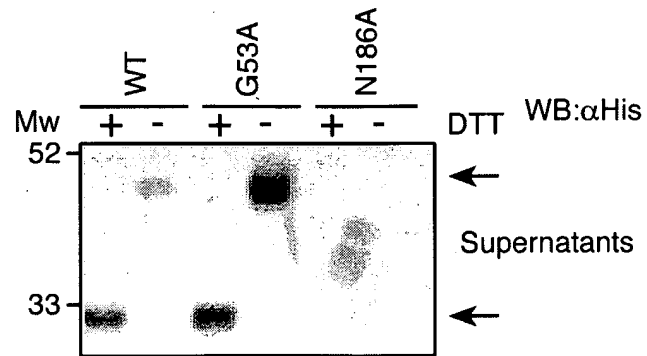
**FIG. 8A**



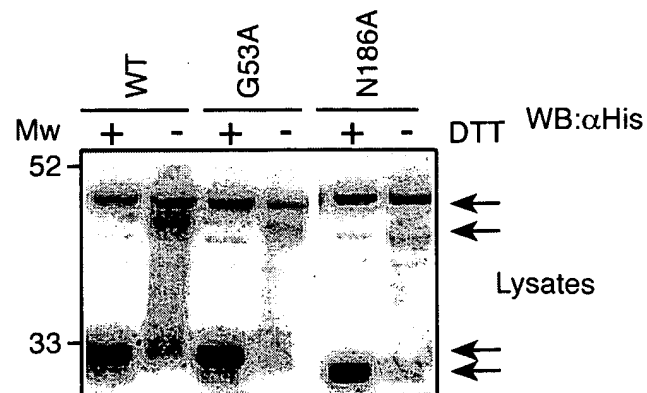
**FIG. 8B**



**FIG. 9A**



**FIG. 9B**



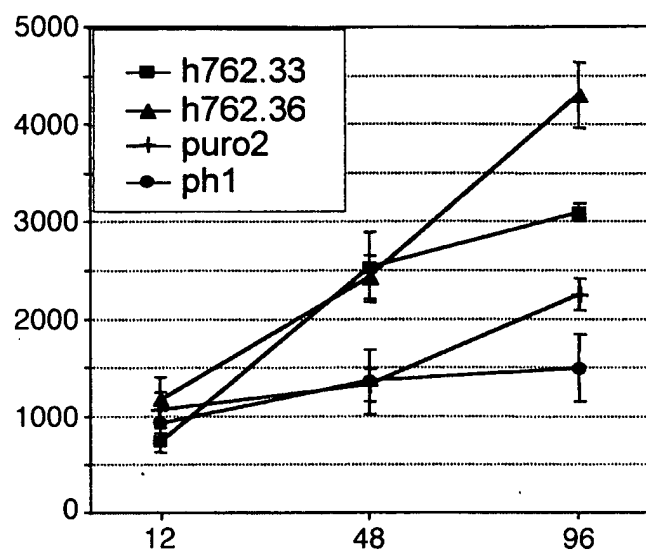
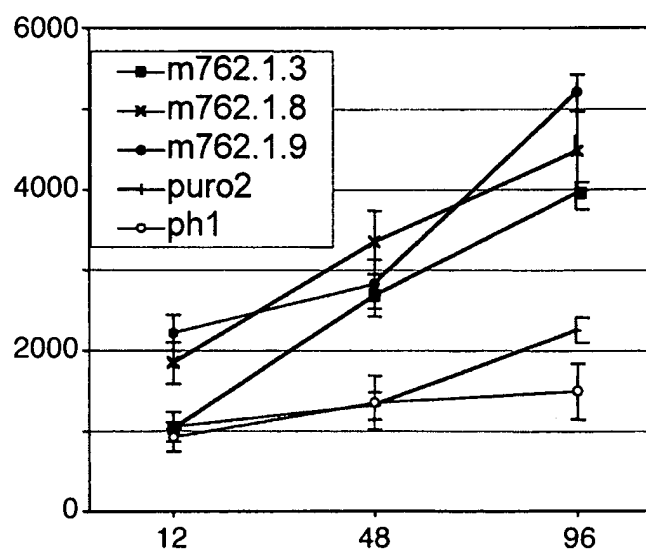
Mw	WT		C55A		C93A		C109A		DTT	
	+	-	+	-	+	-	+	-		
52									←	WB:αHis
33									←	Supernatants

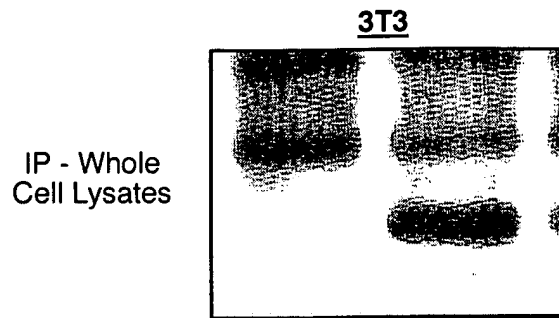
Western blot analysis of His-tagged WT, C55A, C93A, and C109A mutant proteins. The blot shows protein bands for each mutant under DTT (+) and DTT (-) conditions. Molecular weight markers are indicated at 52 and 33 kDa. Arrows on the right indicate the positions of the mutant proteins (WB:αHis) and the lysates.

660 bp  
450 bp

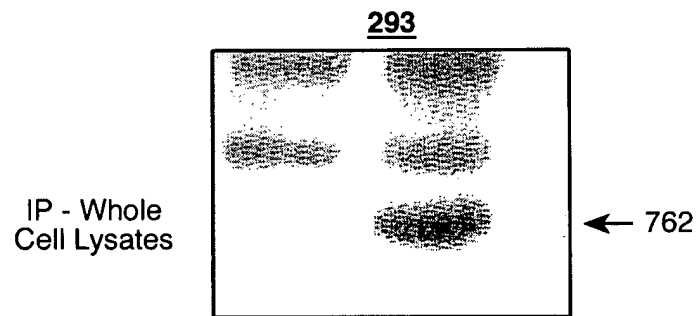
T1 T2 T3 T4 T5 T6 T7 N

762  
RPL19

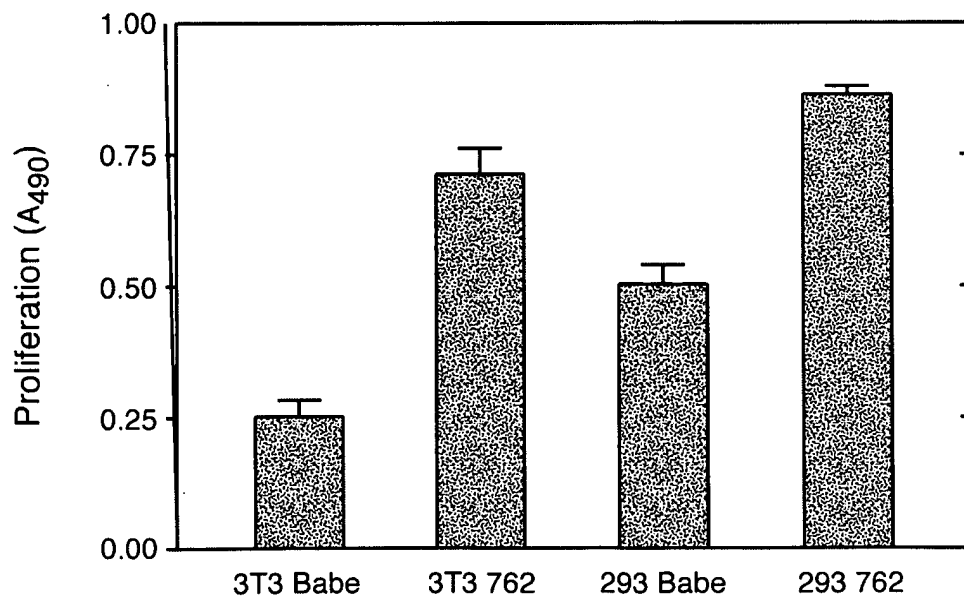
**FIG. 12A****FIG. 12B**



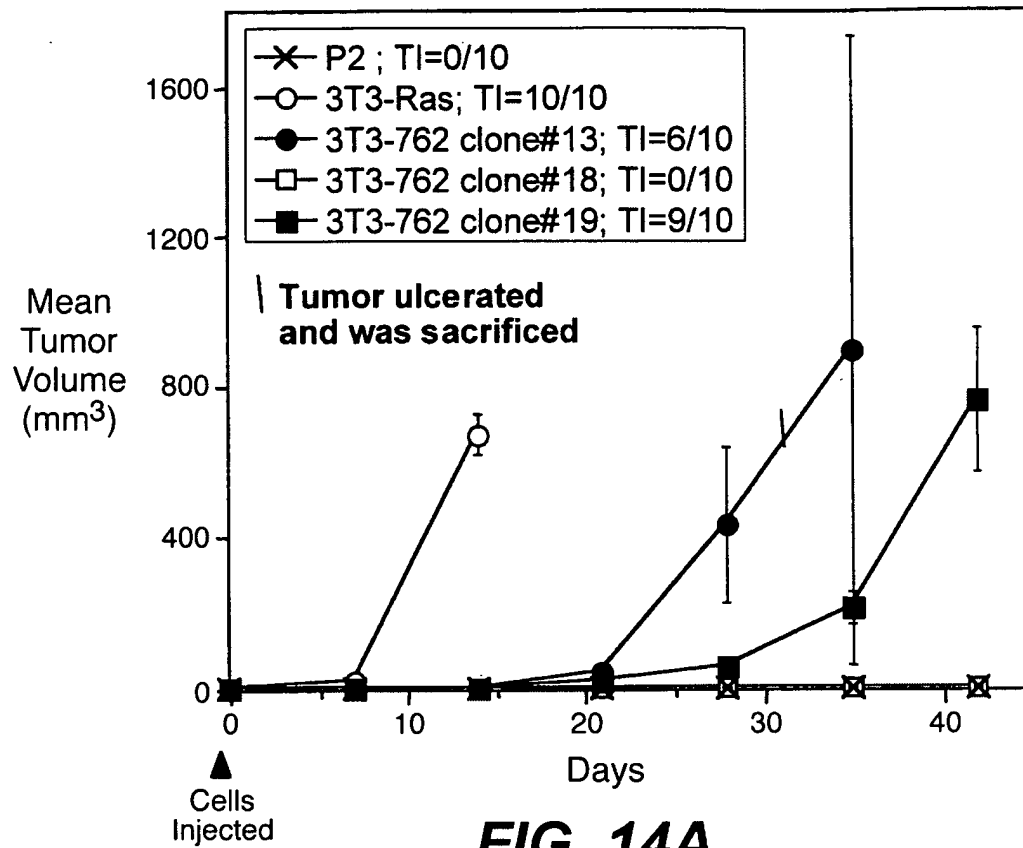
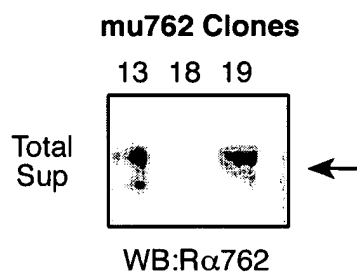
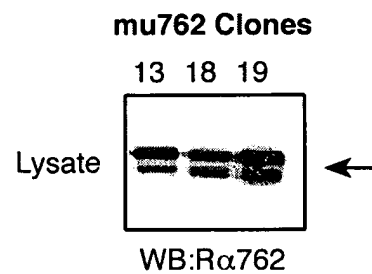
**FIG. 13A**



**FIG. 13B**

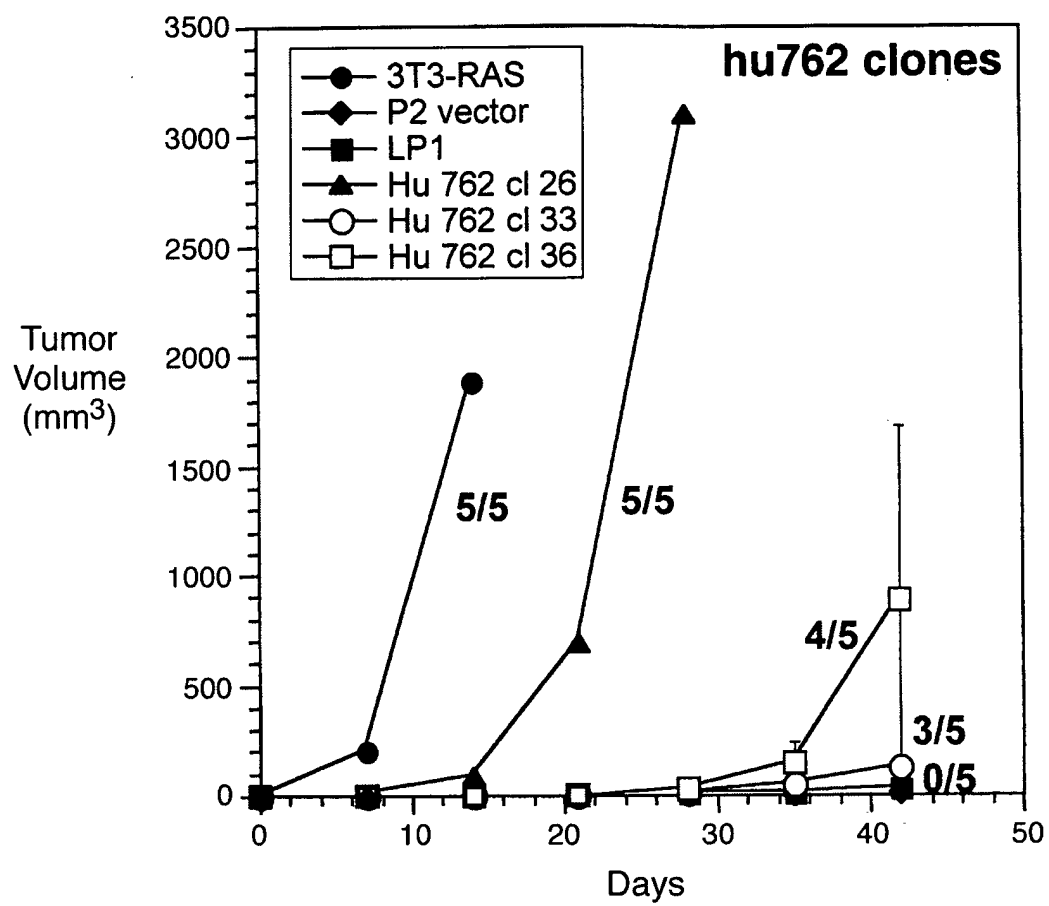


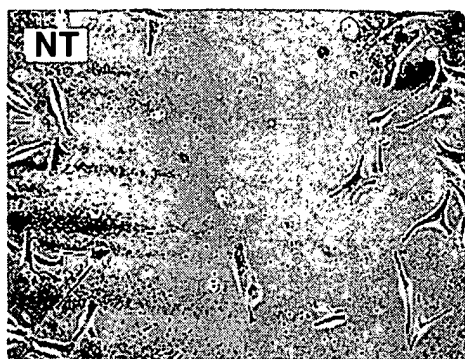
**FIG. 13C**

**FIG. 14A****FIG. 14B****FIG. 14C**



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**FIG. 15**



**FIG. 16A**



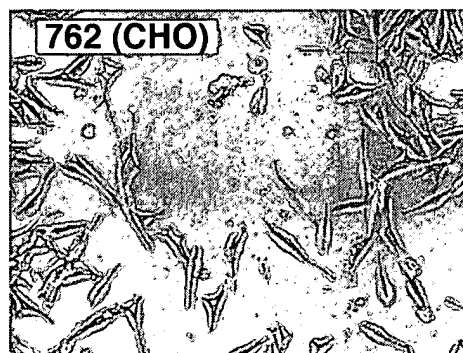
**FIG. 16C**



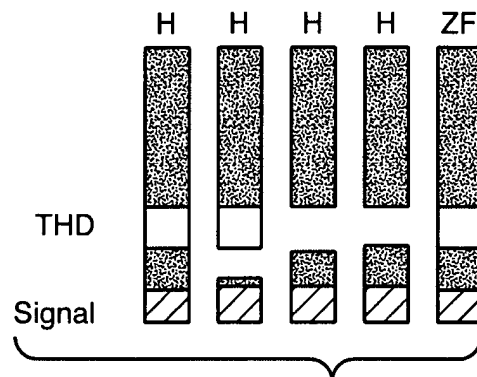
**FIG. 16B**



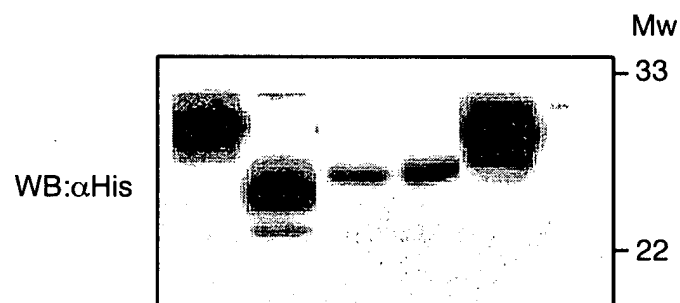
**FIG. 16D**



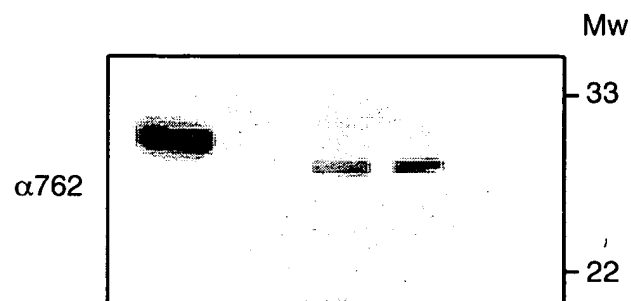
**FIG. 16E**



**FIG. 17A**



**FIG. 17B**



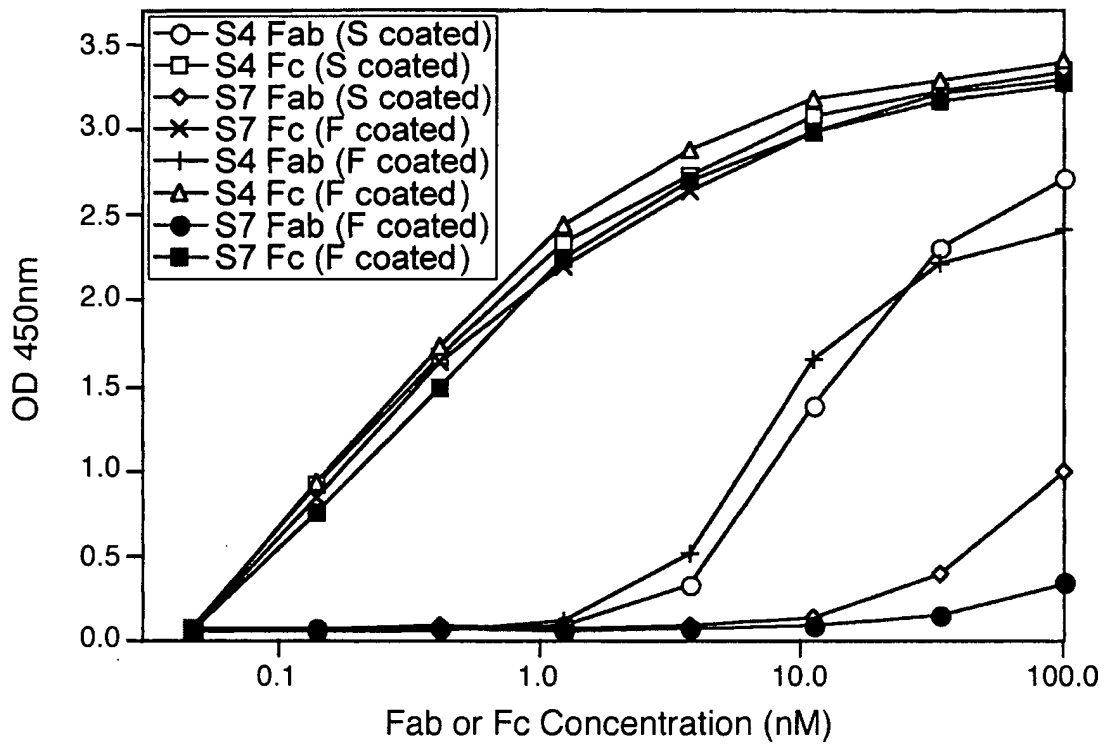
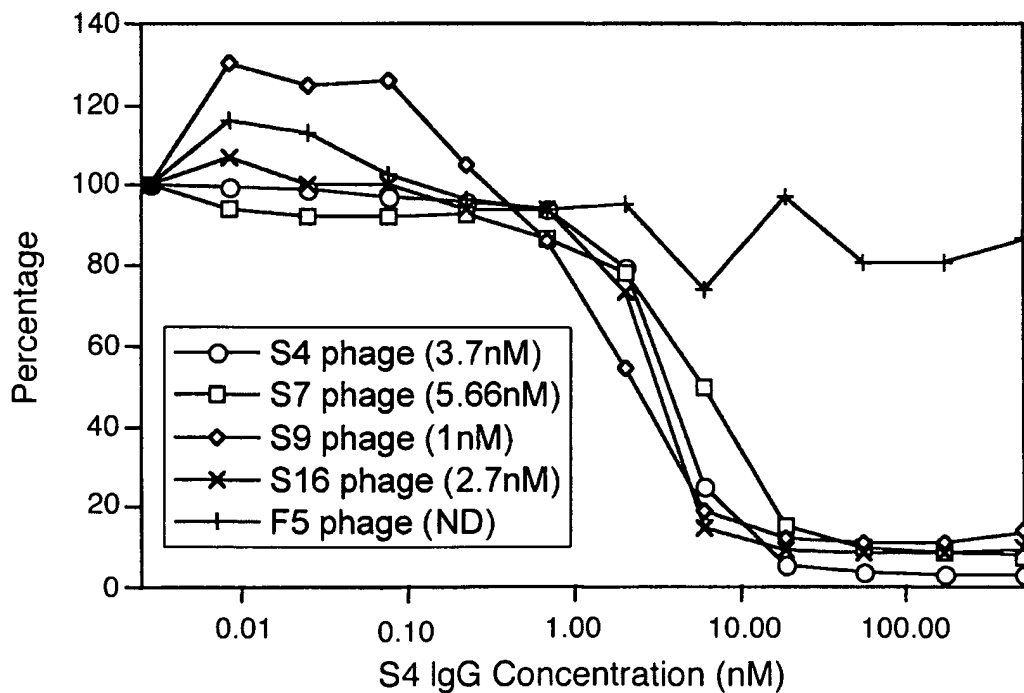
**FIG. 17C**

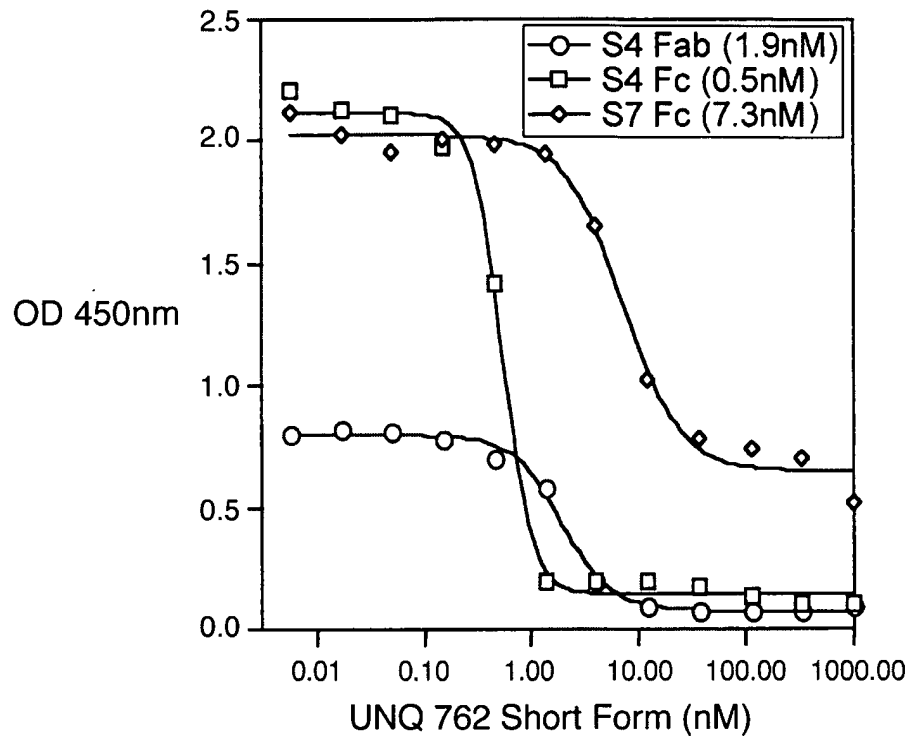
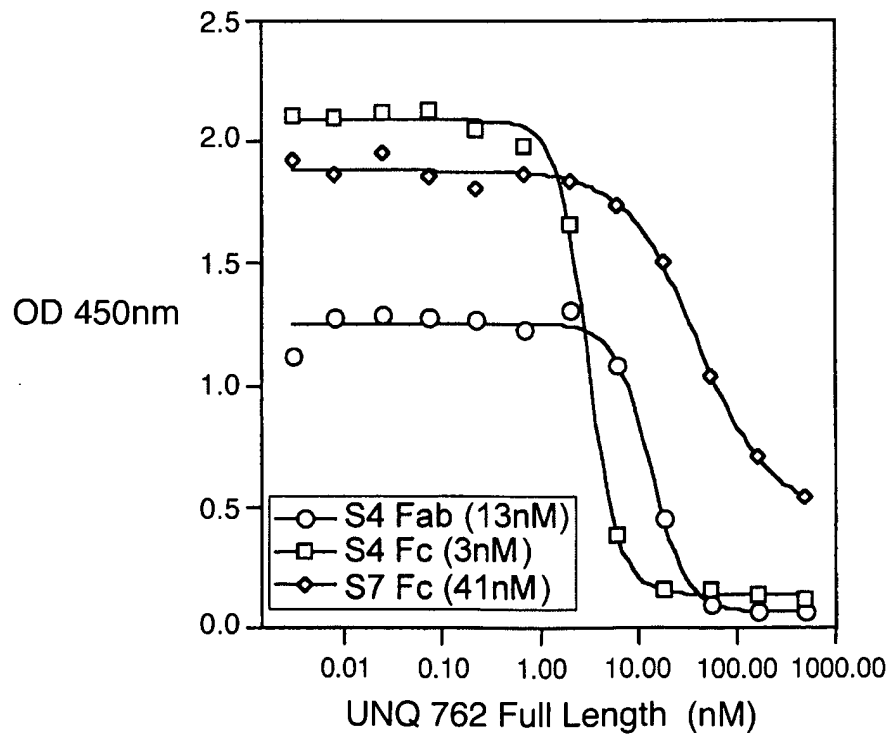
HI					H2													H3													Name
28	29	30	31	32	33	49	50	51	52	52a	53	54	55	56	57	58	92	93	94	95	96	97	98	99	100	100a	100b	100c	101	102	
T	I	S	G	S	D	G	R	I	S	P	Y	G	G	N	T	N	C	A	R	V	G	G	L	K	L	L	-	F	D	Y	S7
T	I	T	N	S	D	A	T	I	Y	P	Y	G	G	Y	T	Y	C	A	R	G	G	G	M	D	G	Y	V	M	D	Y	S16
T	I	N	N	Y	D	G	Y	I	S	P	P	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y	F5
T	I	N	N	Y	D	G	Y	I	S	P	P	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y	F6
T	I	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	S4
T	I	S	N	Y	G	G	R	I	S	P	S	N	G	S	T	Y	C	A	K	C	S	V	R	-	-	-	-	F	A	Y	S9
T	I	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	F13
T	I	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	F47

**FIG. 18**

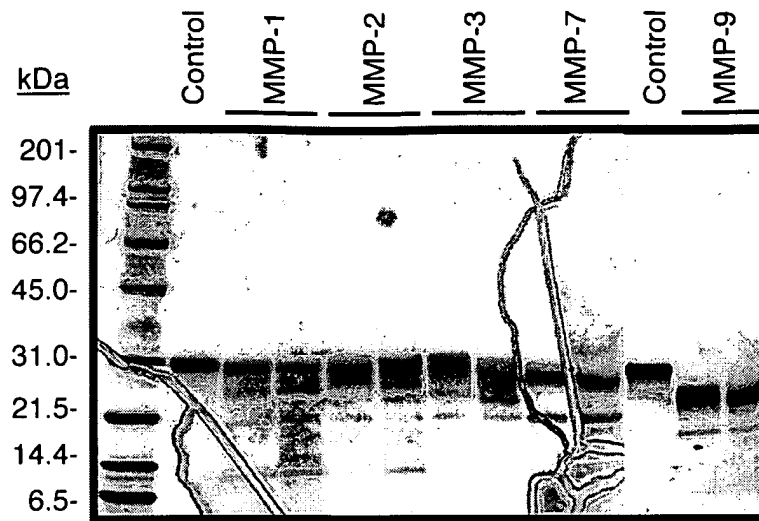
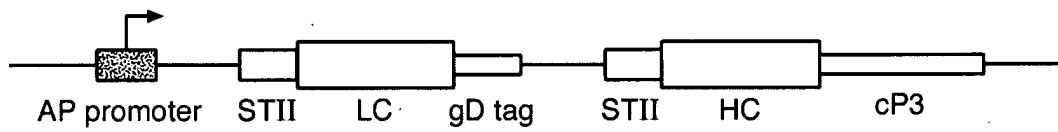
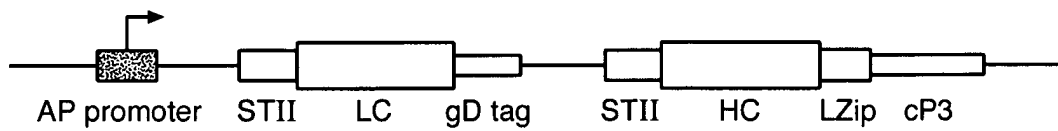
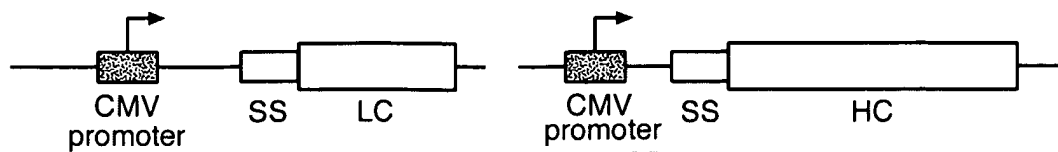
	Phage		Fab		IgG	
S4	762 S/S	762 F/F	762 S/S	762 F/S	762 S/S	762 F/F
	3nM	0.9nM	3.6nM (1.9nM)	32nM	0.5nM	3.1nM
S7	762 S/S	762 F/F	762 S/S	762 F/S	762 S/S	762 F/F
	35nM	2.7nM	113nM	57nM	7.3nM	41nM

**FIG. 21**

**FIG. 19****FIG. 22**

**FIG. 20A****FIG. 20B**

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**FIG. 23****FIG. 24A****FIG. 24B****FIG. 24C****FIG. 24D**

```

1 GAATCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCAFTGCTGA GTTGTATTTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
CTTAAGTTGA ACAGGTATGA AACCTATTCC TTTATGCTG TACTTTTGTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
CTTGACACAC CGGTCCATCT TCGAAACCTC TAATAGGAGT GACGTACGA AGCGTTATAC CCGGTTTTAC TGGTTGTCG CAACTAATA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCTCTGA CGACGATACG GAGTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCACTA
CCGCGGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCACA GCTGTCTATA AGTTGTCACG GCCGAGACTT ATACGCTCTT TGTTTTATT TTTTAATGTA TTTGTAACTA GTACGCAAGT
TTTTCAAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGGTATGTA GAGGTGAGG TGATTTTATG AAAAGAATA TCGCATTTCT TCTTGCATCT ATGTTCTGTTT TTTCTATTGC TACAAATGCC
AGTGCATTTT TCCCATACAT CTCCAATCC ACTAAATAC TTTTCTTAT AGCGTAAAGA AGAAGCTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG
1 M K K N I A F L L A S M F V F S I A T N A
^start of still signal sequence
^met

501 TATCAGATA TCCAGATGAC CCAGTCCCG AGCTCCCTGT CCGCTCTGT GGGCGATAGG GTACCATCA CTGCGGTGC CAGTCAGGAT GTGTCCACTG
ATACGTCTAT AGGTCTACTG GGTGAGGGC TCGAGGGACA GGGGAGACA CCCGTATCC CAGTGGTAGT GGACGGCAG GTCAGTCTTA CACAGGTGAC
22 Y A D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q D V S T A
^start of light chain ^CDR-L1

601 CTCTAGCCTG GTATCAACAG AAACCAGGAA AAGCTCCGAA GCTTCTGATT TACTGGGCAT CCTTCCTCTA CTCTGGAGTC CCTTCTCGCT TCTCTGGTAG
GACATCGGAC CATAGTTGTC TTTGGTCCCT TTCGAGGCTT CGAAGACTAA ATGAGCCGTA GGAAGGAGAT GAGACCTCAG GGAAGAGCGA AGAGACCATC
56 V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G S
^CDR-L2

701 CGGTCCGGG ACGGATTCA CTCTGACCAT CAGCAGTCTG CAGCCGGAAG ACTTCGCAAC TTATTACTGT CAGCAATCTT ATACTACTCC-TCCCACGTTT
GCCAAGGCC TGCCTAAAGT GAGACTGGTA GTCGTACAG GTCGGCTTC TGAAGCTTG AATAATGACA GTCGTTAGAA TATGATGAGG AGGTTGCAAG
89 G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F
^CDR-L3

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**FIG.\_25A**



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801 GGACAGGGTA CCAAGGTGGA GATCAAACGA ACTGTGGGTG CACCACTGTG CCGCCATCTG ATGAGCAGTT GAAATCTGGA ACTGCCTCTG
    CCTGTCCCAT GGTTCACCT CTAGTTTGTG TGACACCGAC GTGGTAGACA GAAGTAGAAG GCGGTAGAC TACTCGTCAA CTTTAGACCT TGACGGAGAC
122 G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V

901 TTGTGTGCT GGTGAATAAC TTCTATCCCA GAGAGGCCAA AGTACAGTGG AAGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA GTGTCACAGA
    AACACACGGA CGACTTATTG AAGATAGGGT CTCTCCGGTT TCATGTCACC TTCCACCTAT TCGGGGAGGT TAGCCCATG AGGTCTCTCT CACAGTGTCT
156 V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E

1001 GCAGGACAGC AAGACAGCA CCTACAGCCT CAGCAGCACC CTGACGCTGA GCAAGCAGA CTACAGAAA CACAAAGTCT AGCCTGCGA AGTCACCCAT
    CGTCCCTGTG TTCCTGTGCGT GGATGTCGGA GTCGTGCTGG GACTGCGACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TCGGACGCT TCAGTGGGTA
189 Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H

1101 CAGGGCTGA GCTGCCCCGT CACAAAGAGC TTCAACAGGG GAGAGTGTGG TGCCAGCTCC GGTATGGCTG ATCCGAACCG TTTCCGGCGT AAGGACCTGG
    GTCCCGGACT CGAGCGGGCA GTGTTTCTCG AAGTTGTCCC CTCTCACACC ACGGTGAGG CCATACCGAC TAGGCTTGGC AAAGCGGCA TTCCTGGACC
222 Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L A
    ^end of light chain, start of gp tag

1201 CATAACTCGA GGCTGATCCT CTACGCCGGA CGCATCGTGG CCCTAGTACG CAAGTTCACG TAAAAGGGT AACTAGAGGT TGAGGTGATT TTATGAAAAA
    GTATTGAGCT CCGACTAGGA GATGCGGCCCT GCGTAGCACC GGGATCATGC GTTCAAGTGC ATTTTTCCTCA TTGATCTCCA ACTCCACTAA AATACITTTT
256 O
-23

1301 GAATATCGCA TTTCTTCTTG CATCTATGTT CGTTTTTTCT ATTGCTACAA ACGCTACGC TGAGGTTTCAG CTGGTGGAGT CTGGCGGTGG CCTGGTGCAG
    CTTATAGCGT AAAGAAGAAC GTAGATACAA GCAAAAAAGA TAACGATGTT TGCGCATGCG ACTCCAAGTC GACCACCTCA GACCGCCACC GGACCACTC
-20 N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G G L V Q
    ^start of heavy chain

1401 CCAGGGGGCT CACTCCGTTT GTCCGTGCGA GCTTCTGGGT TCAACANTAA AGACACCTAT ATACACTGGG TCGGTCAGGC CCCGGGTAG GGCCTGGAAT
    GGTCCTCCCGA GTGAGGCAA CAGGACACGT CGAAGACCGA AGTTGTAATT TCTGTGGATA TATGTGACCC ACGCAGTCCG GGGCCCATTC CCGGACCTTA
14 P G G S L R L S C A A S G F N I K D T Y I H W V R Q A P G K G L E W
    ^CDR-H1

```

M K K  
^start of stII

FIG.. 25B

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1501 GGGTTGCAAG GATTATATCTT ACGAATGGTT ATACTAGATA TGCGATAGC GTCAAGGGCC GTTTCACATAT AAGCGCAGAC ACATCCAAAA ACACAGCCTA
      CCCAACGTTT CTAAATAGGA TGCTTACCAA TATGATCTAT ACGGTATCG CAGTCCCGG CAAAGTGATA TTCGCGTCTG TGTAGTTTTT TGTGTGGGAT
48  V A R I Y P T N G Y T R Y A D S V K G R F T I S A D T S K N T A Y
      ^CDR-H2

1601 CCTACAAATG AACAGCTTAA GAGCTGAGGA CACTGCCGTC TATTATTGTA GCGCTGGGG AGGGACGGC TTCTATGCTA TGGACTACTG GGTCAAGGA
      GGATGTTTAC TTGTGGAATT CTCGACTCCT GTGACGGCAG ATATAACAT CGGCGACCCC TCCCCTGCCG AAGATACGAT ACCTGATGAC CCCAGTTCCT
81  L Q M N S L R A E D T A V Y Y C S R W G G D G F Y A M D Y W G Q G
      ^CDR-H3

1701 ACACTAGTCA CCGTCTCCTC GGCCTCCACC AAGGGCCCAT CCGTCTTCCC CTTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACACGG GCCCTGGGCT
      TGTGATCAGT GGCAGAGGAG CCGGAGGTGG TTCCCGGGTA GCCAGAAGG GACCGTGGG AGGAGTTCT CGTGGAGACC CCCGTGTGCG CGGGACCCGA
114 T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C

1801 GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAAGTCA GGGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTC
      CGGACCAGTT CCTGATGAAG GGGCTTGGCC ACTGCCACAG CACCTTGAGT CCGCGGGACT GGTGCGCGCA CGTGTGGAAG GGCCGACAGG ATGTACAGAG
148 L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S

1901 AGGACTCTAC TCCCTCAGCA GCGTGTGTGAC CGTGCCCTCC AGCAGTTGG GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCGAG CAACACCAAG
      TCCTGAGATG AGGGAGTCGT CGCACCACTG GCACGGGAGG TCGTGGAACC CGTGGTCTG GATGTAGACG TTGCACCTAG TGTTCGGGTC GTTGTGGTTC
181 G L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K

2001 GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAACTC ACCTCAGTGG CCGTGGCTCT GTTCCGGTG ATTTTGATTA TGAAAAGATG GCAAACGCTA
      CAGCTGTTCT TTCAACTCGG GTTTAGAAC A CTGTTTGTAG TGGAGTCACC GCCACCGAGA CCAAGGCCAC TAAAACTAAT ACTTTTCTAC CGTTTGGGAT
214 V D K K V E P K S C D K T H L S G G S G S G D F D Y E K M A N A N

      ^end of heavy chain
      ^start of gene III coat protein (267-end)

2101 ATAAGGGGGC TATGACCGAA AATGCCGATG AAAACGGCT ACAGTCTGAC GCTAAAGGCA AACTTGATTC TGTGCTACT GATTACGGTG CTGCTATCGA
      TATTCCCCCG ATACTGGCTT TTACGGCTAC TTTTGGCGGA TGTACAGACTG CGATTCCGT TTGAACTAAG ACAGCGATGA CTAATGCCAC GACGATAGCT
248 K G A M T E N A D E N A L Q S D A K G K L D S V A T D Y G A A I D

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**FIG.\_25C**

2201 TGGTTTCATT GGTGACGTTT CCGGCCCTTGC TAAATGGTAAT GGTGCTACTG GTGATTTTGC TGGCTCTAAT TCCCAAATGG CTCAACTCGG TGACGGTGAT  
ACCAAAGTAA CCACTGCAAA GCGCGGAACG ATTACCATTA CCACGATGAC CACTAAACG ACCGAGATTA AGGTTTACC GAGTTACAGCC ACTGCCACTA  
281 G F I G D V S G L A N G N G A T G D F A G S N S Q M A Q V G D G D  
2301 AATTCACCTT TAATGAATAA TTTCGGTCAA TATTACCTT CCCTCCCTCA ATCGGTTGAA TGTGCCCCCTT TTGTCTTTAG CGCTGGTAAA CCATATGAAT  
TTAAGTGGAA ATTACTTATT AAAGGCAGTT ATAAATGGAA GGAGGGAGT TAGCCAACTT ACAGCGGGA AACAGAAATC GCGACCATTT GGTATACTTA  
314 N S P L M N N F R Q Y L P S L P Q S V E C R P F V F S A G K P Y E F  
2401 TTTCATTTGA TTGTGACAAA ATAACTTAT TCCGTGGTGT CTTTGGGTTT CTTTATATG TTGCCACCTT TATGTATGTA TTTTCTACGT TTGCTAACAT  
AAAGATAACT AACACTGTTT TATTTGAATA AGGCACCACA GAACGCAAA GAAATATATC AACGGTGGAA ATACATACAT AAAAGATGCA AACGATTGTA  
348 S I D C D K I N L F R G V F A F L L Y V A T F M Y V F S T F A N I  
2501 ACTGCGTAAT AAGAGTCTT ATCATGCCA GTTCTTTTGG CTAGCGCCGC CCTATACCTT GTCTGCCCTC CCGCGTTGG TCGCGGTGCA TGGAGCCGGG  
TGACGCATTA TTCTCAGAA TTAGTACGGT CAAGAAAACC GATCGCGCG GATATGGAA CAGACGGAGG GCGCAACGC AGCGCACGT ACCTCGGCC  
381 L R N K E S O  
2601 CCACCTCGAC CTGAATGAA GCGCGCGCA CCTCGCTAAC GGATTCACCA CTCCAAGAAT TGGAGCCAAAT CAATTCTTGC GGAGAACTGT GAATGGGCAA  
GGTGGAGCTG GACTTACCTT CCGCCGCCGT GGAGCGATTG CTTAAGTGGT GAGGTTCTTA ACCTCGGTTA GTTAAGAAAG CCTCTTGACA CTTACCGCTT  
2701 ACCAACCTT GGCAGACAT ATCATCGCG TCCGCCATCT CCAGCAGCG CACCGCGGC ATCTCGGCA GCGTTGGTC CTGGCCACGG GTGCGCATGA  
TGGTTGGAA CCGTCTTGA TAGGTAGCGC AGGCGTAGA GGTGTCGGC GTGCGCCGC TAGAGCCCGT CGCAACCCAG GACCGGTGCC CACGCGTACT  
2801 TCGTGCTCCT GTCGTTGAG ACCCGGCTAG GCTGGCGGG TTAGCTTACT GGTAGCAGA ATGAATCACC GATACGCGAG CGAACCTGAA GCGACTGCTG  
AGCACGAGGA CAGCAACTCC TGGGCCGATC CGACCGCCCTT ACGGAATGA CCAATCGTCT TACTTAGTGG CTATGCGCTC GCTTGCACTT CGCTGACGAC  
2901 CTGCAAAACG TCTGGACCT GAGCAACAAC ATGAATGGTC TTGCGTTTCC GTGTTTCGTA AAGTCTGGAA ACGCGGAGT CAGCGCCCTG CACCATATG  
GACGTTTTGC AGACGCTGGA CTCGTTGTTG TACTTACCAG AAGCAAAGG CACAAAGCAT TTCAGACCTT TCGCCCTCA GTGCGGGAC GTGTAATAC  
3001 TTCCGGATCT GCATCGCAGG ATGCTGTGG CTACCTGTG GAACACCTAC ATCTGTATTA ACGAAGCGT GGCATTGACC CTGAGTGATT TTTCTCTGGT  
AAGGCCTAGA CGTAGCGTCC TACGACGACC GATGGACAC CTTGTGGATG TAGACATAAT TGCTTCGCA CCGTAACGG GACTCACTAA AAAGAGACCA

**FIG.\_25D**

3101 CCGCCCGCAT CCATACCGCC AGTTGTTTAC CCTCACACAG TTCCAGTAAC CGGGCATGTT CATCATCAGT AACCCGTATC GTGAGCATCC TCTCTCGTTT  
GGCGCGCGTA GGTATGGCGG TCAACAATG GGAGTGTTGC AAGTCAATG GCCCGTACAA GTAGTAGTCA TTGGGCATAG CACTCGTAGG AGAGAGCAAA

3201 CATCGGTATC ATTACCCCA TGAACAGAAA TTCCCCCTTA CACGGAGGCA TCAAGTGACC AAACCGCCCT TAACATGGCC CGCTTTATCA  
GTAGCCATAG TAATGGGGGT ACTTGCTCTT AAGGGGAAT GTGCCTCCGT AGTTCACCTGG TTTGTCTCTT TTTGGCGGGA ATTGTACCGG GCGAAATAGT

3301 GAAGCCAGAC ATTAACGCTT CTGGAGAAAC TCAACGAGCT GGACGGGGAT GAACAGGCAG ACATCTGTGA ATCGCTTCAC GACCACGCTG ATGAGCTTTA  
CTTCGGTCTG TAATGGCAA GACCTCTTTG AGTTGCTCGA CCTGCCCTTA CTTGTCCGTC TGTAGACACT TAGCGAAGTG CTGGTCCGAC TACTCGAAT

3401 CCGCAGGATC CGGAAATTGT AAACGTTTAT ATTTTCTTAA AATTCGGCTT AAATTTTGT TAAATCAGCT CATTTTTTAA CCAATAGGCC GAAATCGGCA  
GGCGTCTTAG GCCTTTTACA TTTGCAATTA TAAACAATTT TTAAGCGCAA TTTAAAAACA ATTTAGTCTGA GTAAAAAATT GGTATCCGG CTTTAGCCGT

3501 AAATCCCTTA TAAATCAAAA GAATAGACCG AGATAGGCTT GAGTGTGTGT CCAGTTTGA ACAAGAGTCC ACTATTAAAG AACGTGGACT CCAACGTCAA  
TTTAGGGAAT ATTTAGTTTT CTATCTGGC TCTATCCAA CTCACAACA GGTCAAACCT TGTCTCAGG TGATAATTTC TTGCACCTGA GGTTCAGTT

3601 AGGCGGAAA ACCGTCTATC AGGGCTATGG CCCACTAGCT GAACCATCAC CCTAATCAAG TTTTGTGGG TCGAGGTGCC GTAAAGCACT AAATCGGAAC  
TCCCGCTTTT TGGCAGATAG TCCCGATACC GGTGTATGCA CTTGTAGTG GGATTAGTTC AAAAAACCC AGCTCCACGG CATTTCTGTA TTTAGCCCTG

3701 CCTAAAGGA GCGCCCGATT TAGAGCTTGA CGGGGAAGC CGCGGAACGT GCGGAGAAAG GAAGGAAGA AAGCGAAGG AGCGGGCGCT AGGGCGCTGG  
GGATTTCCT CGGGGGCTAA ATCTCGAAT GCGCTTTTC GCGCTTTGA CCGCTCTTTC CTTCCCTTCT TTCGCTTTCC TCGCCCGCGA TCCCGCGACC

3801 CAAAGTGTAG GGTACGCTG CGCGTAACCA CCACACCGC CGCGCTTAAT GCGCGCTAC AGGGCGCGTC CGGATCCTGC CTCGCGCTT TCGGTGATGA  
GTTACATCG CCAGTGGAC GCGCATTTGT GGTGTGGCG GCGGAATTA CGCGCGATG TCCCGCGCAG GCCTAGGACG GAGCGGCGAA AGCCACTACT

3901 CGGTGAAAAC CTCTGACACA TGCAGCTCCC GGAGACGGTC ACAGCTTGTG TGTAAAGCGA TGCCGGGAGC AGACAAGCCC GTCAGGGGCG GTCAGCGGGT  
GCCACTTTG GAGACTGTGT ACGTCGAGG CCTCTGCCAG TGTGAAACAG ACATTCGCCT ACGGCCCTCG TCTGTTCGGG CAGTCCCGG CAGTCGCCCA

4001 GTTGGCGGGT GTCGGGGCGC AGCCATGACC CAGTCACTGA GCGATAGCGG AGTGTATACT GGCTTAACTA TCGCGCATCA GAGCAGATTG TACTGAGAGT  
CAACCGCCCA CAGCCCCGCG TCGGTACTGG GTCAGTGCAT CGCTATCGCC TCACATATGA CCGAATTGAT ACGCCGTAGT CTCGTCTAAC ATGACTCTCA

**FIG.\_25E**

4101 GCACCATATG CGGTGTGAAA TACCGCACAG ATGCGPAAGG AGAAAATACC GCATCAGGCG CTCTTCCGCT TCCTCGCTCA CTGACTCGCT GCGTCGGTC  
 CGTGGTATAC GCCACACATT ATGGCGTCTC TACGCATTCC TCCTTTATGG CGTAGTCCG GAGAAGGCGA AGGAGCGAST GACTAGCGA CGCGAGCCAG  
  
 4201 GTTCGGCTGC GCGGAGCGGT ATCAGCTCAC TAGTCGAGTG AGTTTCCGCC ATTATGCCAA TAGTGCTCTT AGTCCCCCTAT TCGCTCCCTTT CTTGTACACT CGTTTTCCGG  
 CAAGCCGACG CCGCTCGCCA TAGTCGAGTG  
  
 4301 AGCAAAAGGC CAGGAACCGT AAAAAGGCGG CGTTGCTGGC GTTTTTCCTAT AGGTCCGCC CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG  
 TCGTTTTCCG GTCCTTGCCA TTTTTCGGC GCAACGACCG CAAAAGGTA TCCGAGGCGG GGGGACTGCT CGTAGTGTTT TTAGCTGCGA GTTCAGTCTC  
  
 4401 GTGGCGAAAC CCGACAGGAC TATAAAGATA CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC TGCCGCTTAC CGGATACCTG  
 CACCGCTTGG GCGTGCTCTG ATATTCTAT GGTCCGCAAA GGGGACCTT CGAGGGAGCA CCGAGAGGA CAAGGCTGGG ACGGCGAATG GCCTATGGAC  
  
 4501 TCCGCTTTC TCCCTTCGGG AAGCGTGGG CTTTCTCAT GCTACGCTG TAGGTATCTC AGTTCGGTGT AGTCTGTTG CTCCAAGCTG GGCTGTGTC  
 AGCGGGAAG AGGGAAGCCC TTCCGACCCG GAAAGAGTAT CGAGTCCGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC GAGGTTCCGAC CCGACACACG  
  
 4601 ACGAACCCC CGTTCAGCCC GACCGCTGG CTTTATCCG TAACATATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC  
 TGCTTGGGG GCAAGTCGG CTGGCGACG GGAATAGGCC ATTGATAGCA GAACTCAGGT TGGGCCATTG TGTGCTGAAT AGCGGTGACC GTCGTCGGTG  
  
 4701 TGCTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGT GCTTAACCTAC GGCTACACTA GAAGGACAGT ATTGTGTATC  
 ACCATGTCC TAATCGTCTC GCTCCATACA TCCGCCACGA TGCTCAAGA ACTTCACCAC CGGATTGATG CCGATGTGAT CTTCCTGTCA TAAACCATAG  
  
 4801 TCGGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG GTAGTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC  
 ACGGAGACG ACTTCGGTCA ATGGAAGCCT TTTTCTCAAC CATCGAGAAC TAGGCCGTTT GTTTGGTGGC GACCATCGCC ACCAAAAAAA CAAACGTTCC  
  
 4901 AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGATTTT  
 TCGTCTAATG CCGCTCTTTT TTTCTTAGAG TTCTTCTAGG AAACTAGAAA AGATGCCCCA GACTGCGAGT CACCTTGCTT TTGAGTGCAA TTCCCTAAAA  
  
 5001 GGTCAATGAGA TTATCAAAAA GGATCTTCAC CTAGATCCTT TTAATATAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC  
 CCAGTACTCT AATAGTTTTT CCTAGAAGTG GATCTAGGAA AATTAAATTT TTAATTCTAA ATTAGTTAG ATTTCATATA TACTCATTTG AACCAGACTG

**FIG.\_25F**

5101 AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT TCGTTTCATCC ATAGTTGCCT GACTCCCCCGT CGTGTAGATA ACTACGATAC  
TCAATGGTTA CGAATTAGTC ACTCCGTGGA TAGAGTCGCT AGACAGATAA AGCAAGTAGG TATCAACGGA CTGAGGGGCA GCACATCTAT TGATGCTATG

5201 GGGAGGGCTT ACCATCTGGC CCCAGTGGTG CAATGATACC GCGAGACCCA CGCTCACCGG CTCAGATTTC ATCAGCAATA AACAGCCAG CCGGAAGGCG  
CCCTCCCGAA TGGTAGACCG GGGTCACGAC GTTACTATGG CGCTCTGGGT GCGACTGGCC GAGGTCTAAA TAGTCGTTAT TTGGTCGGTC GGCCTTCCCG

5301 CGAGGCGAGA AGTGGTCCTG CAACTTTATC CGCCTCCATC CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGGCG  
GCTCGCGTCT TCACCAGGAC GTTGAATAG GCGGAGGTAG GTCAGATAAT TAACAACGGC CTTTCGATCT CATTCATCAA GCGGTCAATT ATCAAACGCG

5401 AACGTTGTTG CCATTGCTGC AGGCATCGTG GTGTCACGCT CGTCGTTTGG TATGGCTTCA TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT  
TTGCAACAAC GGTAAACGAC TCCGTAGCAC CACAGTGCGA GCAGCAAAACC ATACCGAAGT AAGTCGAGGC CAAGGGTTGC TAGTTCCGCT CAATGTACTA

5501 CCCCCATGTT GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAACTA AGTTGGCCGC ACTGTTATCA CTCATGGTTA TGGCAGCACT  
GGGGGTACAA CACGTTTTTT CGCCAATCGA GGAAGCCAGG AGGCTAGCAA CAGTCTTCAT TCAACCCGGC TCACAATAGT GAGTACCAAT ACCGTCGTGA

5601 GCATAAATCT CTTACTGTCA TGCCATCCGT AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGATGCG GCGACCGAGT  
CGTATTAGA GAATGACAGT ACGGTAGGCA TTCTACGAAA AGACACTGAC CACTCATGAG TTGGTTCAGT AAGACTCTTA TCACATACGC CGCTGGCTCA

5701 TGCTCTTGCC CGGCGTCAAC ACGGGATAAT ACCGGGCCAC ATAGCAGAAC TTTTAAAGTG CTCATCATTG GAAAACGTTT TTCGGGGCGA AAACCTCTCA  
ACGAGAACGG GCGGCAGTTG TGCCCTATTA TGGCGCGGTG TATCGTCTTG AAATTTTAC GAGTAGTAAC CTTTTGCAAG AAGCCCCGCT TTTGAGAGTT

5801 GGATCTTACC GGTGTGAGA TCCAGTTCGA TGTAACCCAC TCGTGACCC AACGATCTT CAGCATCTTT TACTTTCACC AGCGTTCTG GGTGAGCAAA  
CCTAGAATGG CGACAACCTCT AGGTCAAGCT ACATTGGGTG AGCACGTGGG TTGACTAGAA GTCGTAGAAA ATGAAAGTGG TCGCAAGAC CCACTCGTGT

5901 AACAGGAAG CAAATGCCG CAAAAAGGG AATAAGGGG ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTTATCAG  
TTGTCTCTCC GTTTTACGGC GTTTTTTCCC TTATTCCCCT TGTCCTTTA CAACCTATGA GTATGAGAAG GAAAAAGTTA TAATACTTC GTAAATAGTC

6001 GGTATTGTC TCATGAGCGG ATACATATTT GAATGATTTT AGAAAAATAA ACAATAGGG GTTCCCGGCA CATTTCCCGG AAAAGTGCCA CCTGACGCT  
CCAATACAG AGTACTCGCC TATGTATAAA CTTACATAAA TCTTTTTTAT TGTTTATCCC CAAGCGCGT GTAAAGGGG TTTTCACGGT GGACTGCAGA

**FIG.\_25G**

6101 AAGAAACCAT TATTATCATG ACATTAACCT ATAAAAATAG GCGTATCACG AGGCCTTTC GTCTTCAATA CAGGTAGACC TTTCGTAGAG ATGTACAGTG  
TTCTTTGGTA ATAAATAGTAC TGTAATTGGA TATTTTATC CGCATAGTGC TCCGGAAAG CAGAAGTTAT GTCCATCTGG AAAGCATCTC TACATGTAC

6201 AAATCCCCGA AATTATACAC ATGACTGAAG GAAGGGAGGT CGTCATTCCC TGCCGGGTTA CGTCACCTAA CATCACTGTT ACTTTAAAAA AGTTTCCACT  
TTTAGGGGCT TTAATATGTG TACTGACTTC CTTCCTCCGA GCAGTAAGGG ACGGCCCAAT GCAGTGGATT GTAGTGACAA TGAAATTTTT TCARAGGTGA

6301 TGACACTTTG ATCCCTGATG GAAAACGCAT AATCTGGGAC AGTAGAAGG GCTTCATCAT ATCAAAATGCA ACGTACAAAG AAATAGGGCT TCTGACCTGT  
ACTGTGAAC TAGGGACTAC CTTTGGCGTA TTAGACCCCTG TCATCTTTCC CGAAGTAGTA TAGTTTACGT TGCATGTTTC TTTATCCCGA AGACTGGACA

6401 GAAGCAACAG TCAATGGGCA TTTGTATAAG ACAACTATC TCACACATCG ACAACCAAT ACAATACAGG TAGACCTTTC GTAGAGATGT ACAGTGAAT  
CTTCGTTGTC AGTTACCCGT AAACATATTC TGTTTGATAG AGTGTGTAGC TGTTTGGTTA TGTTATGTCC ATCTGGAAG CATCTCTACA TGTCACTTTA

6501 CCCGAAATT AFACACATGA CTGAAGGAAG GGAGCTCGTC ATTCCCTGCC GGGTTACGTC ACCTAACATC ACTGTTACTT TAAAAAAGTT TCCACTTGAC  
GGGGCTTAA TATGTGTACT GACTTCCTTC CCTCGAGCAG TAAGGGACGG CCCATGCAG TGGATGTAG TGACAATGAA ATTTTTCAA AGGTGAACTG

6601 ACTTTGATCC CTGATGGAAA ACGCATATC TGGGACAGTA GAAAGGGGTT CATCATATCA AATGCAACGT ACAAGAAT AGGGCTTCTG ACCTGTGAAG  
TGAACACTAGG GACTACCTTT TCGGTATTAG ACCCTGTCTAT CTTTCCCGAA GTAGTATAGT TTACGTTGCA TGTTTCTTTA TCCCGAAGAC TGGACACTTC

6701 CAACAGTCAA TGGGCATTG TATAAGACAA ACTATCTCAC ACATCGACAA ACCAATACAA TCTACAGGTA GACCTTTCGT AGAGATGTAC AGTGAATCC  
GTTGTCAGTT ACCCGTAAAC ATATTCTGTT TGATAGAGTG TGTAGCTGTT TGTTATGTT AGATGTCCAT CTGGAAGCA TCTCTACATG TCACTTTAGG

6801 CCGAAATTAT ACACATGACT GAAGGAAGGG AGCTCGTCTAT TCCCTGCGG GTTACGTCAC CTAACATCAC TGTTACTTTA AAAAAGTTTC CACTTGACAC  
GGCTTTAATA TGTGTACTGA CTTCTCTCCC TCGAGCAGTA AGGGACGGCC CAATGCAGTG GATTGTAGTG ACAATGAAAT TTTTTCAAAG GTGAACCTGT

6901 TTTGATCCCT GATGGAAAAC GCATAATCTG GGACAGTAGA AAGGGCTTCA TCATATCAA TGCAACGTAC AAAGAATAG GGCTTCTGAC CTGTGAAGCA  
AACTAGGGA CTACCTTTTG CGTATTAGAC CCTGTCTACT TTCCCGAAGT AGTATAGTTT ACGTGTCATG TTTCTTTATC CCGAAGACTG GACACTTCGT

7001 ACAGTCAATG GGCATTGTA TAAGACAAAC TATCTCACAC ATCGACAAAC CAATACAATC  
TGTCAGTTAC CCGTAAACAT ATTCTGTTTG ATAGAGTGTG TAGCTGTTTG GTTATGTTAG

**FIG.. 25H**

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1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCC AAAAGAAGA AGAGTCGAAT
  CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGCTCTG TACTTTTAG AGTAACGACT CAACAATAAA TTGGAACGGG TTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACACGG GTTGATTGAT CAGGTAGAGG
  CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTACGA AGCGTTATAC CGCGTTTAC TGGTTGTCGC CAACTAATA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAG CCCGATGCCA GCATTCCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
  CCGCGGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCACA GCTGTCTATA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTATT TTTTAATGTA TTTGTAATA GTACGCAAGT
  TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAATA AGGTATGTA GAGTTTGAGG TGATTTTATG AAAAGAATA TCACATTTCT TCTTGCATCT ATGTTCTGTTT TTTCTATTGC TACAAATGCC
  AGTGCATTTT TCCCATACAT CTCCAATCC ACTAAATAC TTTTCTTAT AGCGTAAAGA AGAAGCTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG

1 M K K N I A F L L A S M F V F S I A T N A
  ^start of still sequence

501 TATGCATCCG ATATCCAGAT GACCCAGTCC CCGAGTCCC TGTCGCCCTC TGTTGGCGAT AGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTCTCCA
  ATACGTAGGC TATAGGTCTA CTGGGTGAGG GGCTCGAGG ACAGCCGCTA TCCCAGTGGT AGTGGACGGC ACGTCTAGTC CTACACAGGT

22 Y A S D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q D V S T
  ^light chain start ^CDR-L1

601 CTGCTGTAGC CTGGTATCAA CAGAAACCAG GAAAAGTCC GAAGTTCTG ATTTACTCGG CATCCTTCCT CTACTCTGGA GTCCCCTCTC GCTTCTCTGG
  GACGACATCG GACCATAGTT GTCTTTGCTC CTTTTCGAGG CTTTCAAGAC TAAATGAGCC GTAGGAAGGA GATGAGACCT CAGGGAAGAG CGAAGAGACC

56 A V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G
  ^CDR-L2

701 TAGCGGTTCC GGGACGGATT TCACTCTGAC CATCAGCAGT CTGACGCCGG AAGACTTCG AACTTATTAC TGTACGCAAT CTTATACTAC TCCTCCCACG
  ATCGCCAAGG CCCTGCCTAA AGTGAGACTG GTAGTCTGTA GACGTGCGCC TTTTGAAGCG TTGAATAATG ACAGTCGTTA GAATATGATG AGGAGGTGC

89 S G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T
  ^CDR-L3

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**FIG.\_26A**



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801 TTCCGACAGG GTACCAAGGT GGAGATCAAA CGAACTGTGG CTGCACCATC TGTCTTCATC TTCCCGGCAT CTGATGAGCA GTTGAAATCT GGAAGTGCCT
AAGCCTGTCC CATGGTTCCA CCTCTAGTTT GCTTGACACC GACGTGGTAG ACAGAAGTAG AAGGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGGA
122 F G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S

901 CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC CAAAGTACAG TGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG AGAGTGTAC
GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG GTTTCATGTC ACCTTCCACC TATTGCGGGA GGTTAGCCCA TTGAGGGTCC TCTCACAGTG
156 V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T

1001 AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC ACCCTGAGC TGAGCAAGC AGACTAGCAG AAACACAAAG TCTACGCCCT CGAAGTCAAC
TCTCGTCTGT TCGTTCTCTGT CGTGCATGTC GGAGTCGTGC TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG
189 E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T

1101 CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTCAACA GGGGAGAGTG TGGTGCCAGC TCCGGATGG CTGATCCGAA CCGTTTCCGC GGTAAAGGACC
GTAGTCCCGG ACTCGAGCGG GCAGTGTTC TCGAAGTTGT CCCCTCTCAC ACCACGGTCG AGGCCATACC GACTAGGCTT GGCAAAAGCG CCATTCCTGG
222 H Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L
^end of light chain, start of gD tag

1201 TGGCATAACT CGAGGCTGAT CCTCTACGCC GGACGCATCG TGGCCCTAGT ACACAAGTTC ACGTAAAAG GGTAACTAGA GGTGAGGTG ATTTATATGA
ACCGTATTGA GCTCCGACTA GGAGATGCGG CCGCGTAGC ACCGGGATCA TCGGTTCAAG TGCATTTTTC CCATTGATCT CCAACTCCAC TAAATACTT
256 A O
^start of stII

1301 AAAGAATATC GCATTCTTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGGCTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG
TTTCTTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTTGGCGAT CGGACTCCAA GTCGACCACC TCAGACCGCC ACCGGACCAC
-21 K N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G L V
^start of heavy chain

1401 CAGCCAGGGG GCTCACTCCG TTTGTCTCTGT GCAGCTTCTG GCTTCAACAT TAAAGACACC TATAVACACT GGTGTCGTCA GGCCCCGGGT AAGGGCCTGG
GTGCTGTCCTC CGAGTGAGGC AAACAGGACA CGTCGAAGAC CGAAGTTTGA ATTTCTGCG ATATATGTGA CCCAGCAGT CCGGGGCCCA TTCCCGGACC
13 Q P G G S L R L S C A A S G F N I K D T Y I H W V R Q A P G K G L E
^CDR-H1

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FIG.\_26B

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1501 AATGGGTTGC AAGGATTAT CCTACGAATG GTTATACTAG ATATGCCGAT AGCGTCAAGG GCCGTTTCAC TATAAGCGCA GACACATCCA AAAACACAGC
TTACCCAACG TTCCTAATAA GGATGCTTAC CAATATGATC TATACGGCTA TCGCAGTTCC CGGCAAGTG ATATTCCGGT CTGTGTAGGT TTTTGTGTGG
47 W V A R I Y P T N G Y T R Y A D S V K G R F T I S A D T S K N T A
^CDR-H2

1601 CTACCTACAA ATGAACAGCT TAAGAGTGA GGACACTGCC GTCTATTATT GTAGCCGCTG GGGAGGGGAC GGCTTCTATG CTATGGACTA CTGGGGTCAA
GATGGATGTT TACTTGTGCA ATTCTGACT CCTGTGACGG CAGATAATAA CATCGGGAC CCCTCCCCTG CCGAAGATAC GATACCTGAT GACCCAGTT
80 Y L Q M N S L R A E D T A V Y Y C S R W G G D G F Y A M D Y W G Q
^CDR-H3

1701 GGAACACTAG TCACCGCTC CTCGGCCTCC ACCAAGGGCC CATCGGTCTT CCCCTTGGCA CCTCCTCCA AGAGCACTC TGGGGGCACA GCGGCCCTGG
CCTTGTGATC AGTGGCAGAG GAGCCGGAGG TGGTTCCCGG GTAGCCAGAA GGGGGACCGT GGGAGGAGGT TCTCGTGGAG ACCCCCGTGT CGCCGGGACC
113 G T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G

1801 GCTGCCTGGT CAAGGACTAC TTCCCGGAAC CGGTGACGGT GTCGTGGAAC TCAGGCGCCC TGACCAGCGG CGTGCAACACC TTCCCGGCTG TCCTACAGTC
CGACGGACA GTTCTGTGAG AAGGGCTTG GCCACTGCCA CAGCACCTTG AGTCCGCGGG ACTGCTGCC GCACGRTGG AAGGCCGAC AGGATGTCAG
147 C L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S

1901 CTCAGGACTC TACTCCCTCA GCAGCGTGGT GACCGTGCCC TCCAGCAGCT TGGGCACCCA GACCTACATC TGCAACCTGA ATCACAAGCC CAGCAACACC
GAGTCCTGAG ATGAGGGAGT CGTCGCACCA CTGGCACGGG AGGTCGTCGA ACCCGTGGGT CTGGATGTAG ACGTTGCACT TAGTGTTCGG GTCGTTGTGG
180 S G L Y S L S S V V T V P S S L G T Q T Y I C N V N H K P S N T

2001 AAGGTCGACA AGAAGTTGA GCCCAATCT TGTGACAAA CTCACGGCCG CATGAACAG CTAGAGGACA AGGTCGAAGA GCTACTCTCC AAGAACTACC
TTCCAGCTGT TCTTTCACT CGGGTTTAGA ACACTGTTTT GAGTCCCGGC GACTTTGTC GATCTCCTGT TCCAGCTTCT CGATGAGAGG TTCTTGATGG
213 K V D K K V E P K S C D K T H G R M K Q L E D K V E L L S K N Y H
^end of heavy chain, start of leucine zipper

2101 ACCTAGAGAA TGAAGTGCA AGACTCAAAA AACTTGTGCG GGAGCGCGGA AAGCTTAGTG GCGGTGGCTC TGGTCCGGT GATTTTGATT ATGAAAAGAT
TGGATCTCTT ACTTCACCGT TCTGAGTTTT TTGAACAGCC CCTCGCGCCT TTGGAATCAC CGCCACCGAG ACCAAGGCCA CTAATACTAA TACTTTCTA
247 L E N E V A R L K K L V G E R G K L S G G S G S G D F D Y E K M
^end of leucine zipper, start of gene III coat protein (267-end)^

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**FIG.\_26C**

2201 GGCAACCGCT AATAAGGGG CTATGACCGA AATGCCGAT GAAAACGGC TACAGTCTGA CGCTAAGGC AAACCTGATT CTGTCGCTAC TGATTACGGT  
 CCGTTTGGGA TTATTCCCCC GATACTGGCT TTATACGGCTA CTTTTCGGCG ATGTCAGACT CGGATTTCCG TTGTGACTAA GACAGCGATG ACTAATGCCA  
 280 A N A N K G A M T E N A D E N A L Q S D A K G K L D S V A T D Y G  
 2301 GCTGCTATCG ATGGTTTCAT TGGTGACGTT TCCGGCCTTG CTAATGGTAA TGGTGCTACT GGTGATTTTG CTGGCTCTAA TTCCCAAATG GCTCAAGTCG  
 CGACGATAGC TACCRAAGTA ACCACTGCAA AGGCCGGAAC GATTACCATT ACCACGATGA CCACCTAAAC GACCGAGATT AAGGTTTAC CGAGTTCAGC  
 313 A A I D G F I G D V S G L A N G N G A T G D F A G S N S Q M A Q V G  
 2401 GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCCGTCA ATATTACCT TCCCTCCCTC AATCGGTTGA ATGTCGCCCT TTGTCTTTTA GCGCTGGTAA  
 CACTGCCACT ATTAAGTGA AATTACTTAT TAAAGGCAGT TATAAATGGA AGGAGGGAG TTAGCCCACT TACAGCGGA AACAGAAAT CCGGACCAT  
 347 D G D N S P L M N N F R Q Y L P S L P Q S V E C R P F V F S A G K  
 2501 ACCATATGAA TTTTCTATTG ATTGTGACAA AATAAACTTA TTCCGTGGTG TCTTTGCGTT TCTTTTATAT GTTGCCACCT TTATGTATGT ATTTCTTACG  
 TGGTATACCT AAGAGATAAC TAACACTGTT TTATTGTAAT AAGGCACCCAC AGAAACGCAA AGAAATATA CAACGGTGGA AATACATACA TAAAGATGC  
 380 P Y E F S I D C D K I N L F R G V F A F L L Y V A T F M Y V F S T  
 2601 TTTGTACA TACTGCGTAA TAAGGAGTCT TAATCATGCC AGTTCTTTTG GCTAGCGCG CCCTATACCT TGTCGCTC CCCGGGTGC GTCCGGGTGC  
 AAACGATTGT ATGACGCATT ATTCCTCAGA ATTAGTACGG TCAAGAAAC CGATCGCGC GGGATATGGA ACAGACGGAG GGGCGCAACG CAGCGCCACG  
 413 F A N I L R N K E S O  
 2701 ATGGAGCCG GCCACCTCGA CCTGAATGGA AGCCGCGGC ACCTCGCTAA CGGATTACCC ACTCCAAGAA TTGGAGCCAA TCAATTCTTG CCGAGAATCG  
 TACCTCGGC CGGTGGAGCT GGACTTACCT TCGGCGCGC TGGAGCGATT GCCTAAGTGG TGAGGTCTCT AACCTCGGT AGTTAAGAAC GCCTCTTGAC  
 2801 TGAATGCGCA AACCAACCCT TGGCAGAACA TATCCATCGC GTCCGCCATC TCCAGCAGCC GCACGCGCG CATCTCGGC AGCCTGGGT CCTGGCCACG  
 ACTTACGGT TTGGTTGGGA ACCGCTTGT ATAGTAGCG CAGGCGGTAG AGGTGCTCG CGTGCGCCG GTAGAGCCG TCGCAACCCA GGACCGGTGC  
 2901 GGTGCGCATG ATCGTGTCC TGTCGTTGAG GACCCGGCTA GGCTGGCGG GTTGCCCTTAC TGGTTAGCAG AATGAATCAC CGATACCGA GCGAACGTGA  
 CCACGCGTAC TAGCACGAG ACAGCAACTC CTGGCCCGAT CCGACCGCC CAACGGAATG ACCAATCGTC TTACTTAGTG GCTATGCGT CGCTTGCACT  
 3001 AGCGACTGCT GCTGCAAAAC GTCTGGGACC TGAGCAACAA CATGAATGGT CTTGGTTTC CGTGTTCCT AAAGTCTGGA AACGGGAAG TCAGGCGCCT  
 TCGCTGACGA CGACGTTTG CAGACGCTGG ACTCGTTGTT GACTTACCA GAAGCCAAAG GCACAAAGCA TTTCAGACCT TTGCGCCTTC AGTCGCGGGA

**FIG.\_26D**

3101 GCACCATAT GTTCCGGATC TGCATCGCAG GATGCTGCTG GCTACCCCTGT GGRACACCTA CATCTGTATT AACGAAGCG TGGCATTTGAC CCTGAGTGAT  
CGTGGTAATA CAAGGCCTAG ACGTAGCGTC CTACGACGAC CGATGGGACA CCTGTGGAT GTAGACATAA TTGCTTCGG ACGTAAC TG GACTCACTA

3201 TTTTCTCTGG TCCCGCCGCA TCCATACCGC CAGTTGTTTA CCTCACAAC GTTCCAGTAA CCGGGCATGT TCATCATCAG TAACCCGTAT CGTGAGCATC  
AAAAGAGACC AGGGCGCGT AGGTATGGC GTCAACAAT GGGAGTGTG CAAGTCAAT GGCCCGTACA AGTAGTAGTC ATTGGGCATA GCACTCGTAG

3301 CTCTCTCGTT TCATCGGTAT CATTACCCC ATGAACAGAA ATTCCCCCTT ACACGGAGC ATCAAGTGAC CAAACAGGAA AAAACCGCC TTAACATGGC  
GAGAGAGCAA AGTAGCCATA GTAATGGGG TACTTGTCTT TAAGGGGAA TGTGCTCCG TAGTTCAC TGTTGTCTT TTTTGGCGG AATTGTACCG

3401 CCGCTTTATC AGAAGCCAGA CATTACCGT TCTGGAGAAA CTCACAGAGC TGGACGCGGA TGAACAGGCA GACATCTGT AATCGCTTCA CGACCACGCT  
GGCGAAATAG TCTTCGGTCT GTAATTGCCA AGACCTCTT GAGTTGCTCG ACCTGGCCT ACTGTCCGT CTGTAGACAC TTAGCGAAGT GCTGGTGGCA

3501 GATGAGCTTT ACCGCAGGAT CCGGAAATTG TAAACGTTAA TATTTTGTTA AAATTCGCGT TAAATTTTG TTAATCAGC TCATTTTTTA ACCAATAGGC  
CTACTCGAAA TGGCGTCTTA GGCCTTTAAC ATTTGCAATT ATAAACAAT TTTAAGCGCA ATTTAAAAC AATTAGTTCG AGTAAAAAT TGGTTATCCG

3601 CGAATCGGC AAAATCCCCTT ATAAATCAA AGAATAGACC GAGATAGGTT TGACTGTGT TCCAGTTTGG AACAAAGATC CACTATTAAA GAACGTGGAC  
GCTTAGCCG TTTTAGGGAA TATTTAGTTT TCTTATCTGG CTCTATCCCA ACTCACAACA AGTCAAACC TTGTTCTCAG GTGATAATTT CTTCACCTG

3701 TCCAACGTCA AAGGGCGAAA AACCGTCTAT CAGGGCTATG GCCACTACG TGAACCATCA CCTAATCAA GTTTTTTGGG GTCGAGGTGC CGTAAAGCAC  
AGGTGTCAGT TTCCCGCTTT TTGGCAGATA GTCCCGATAC CGGTGATGC ACTTGGTAGT GGGATTAGTT CAAAAAACCC CAGCTCCAG GCATTTCTGTG

3801 TAAATCGGA CCTAAAGG AGCCCCCGAT TTAGAGCTTG ACGGGGAAAG CCGCGGAACG TGCGGAGAAA GGAAGGGAAG AAAGCGAAA GAGCGGGCGC  
ATTTAGCCTT GGGATTCCC TCGGGGGCTA AATCTCGAAC TGCCCCCTTC GSCCGCTGC ACCCTCTTT CCTTCCCTTC TTTCGCTTTC CTCGCCCGG

3901 TAGGGCGCTG GCAAGTG TAG CCGTCACGCT CCGCGTAAAC ACCACACCCG CCGCGCTTAA TGCGCCGCTA CAGGGCGCGT CCGGATCCTG CCTCGCGCGT  
ATCCCGCGAC CGTTCACATC GCCAGTCCA CCGCATTTGG TGGTGTGGG GCGCGGAATT ACGGGCGAT GTCCCGCGCA GGCCTAGGAC GGAGCGCGCA

4001 TTCGGTGATG ACGGTGAAA CCTCTGACAC ATGCAGCTCC CCGAGACGGT CACAGCTGT CTGTAAGCG ATGCCGGGAG CAGACAAGCC CGTCAGGGCG  
AAGCCACTAC TGCCACTTTT GGAGACTGTG TACGTGAGG GCCTCTGCCA GTGTGGAACA GACATTGCC TACGGCCCTC GTCTGTTCG GCAGTCCCGC

4101 CGTCAGCGG TGTGGCGGG TGTCCGCGG CAGCCATGAC CCAGTCACGT AGCGATAGCG GAGTGTATAC TGGCTTAAT ATGCCGCATC AGAGCAGATT  
GCACTCGCC ACAACCGCC ACAGCCCCG GTCGGTACTG GGTCACTGCA TCGCTATCGC CTCACATATG ACCGAATTGA TACGCCGTAG TCTCGTCTAA

**FIG.\_26E**

4201 GTACTGAG TGCACCATAT GCGGTGTGAA ATACCGCACA GATCGGTAAG GAGAAAATAC CGCATCAGGC GCTCTTCCGC TTCTTCGCTC ACTGACTCGC  
CATGACTCTC ACGTGGTATA CGCCACACTT TATGGCGTGT CTACGCCATT CTCTTTTATG CGGTAGTCCG CGAGAGGCG AAGGAGCGAG TGACTGAGCG

4301 TCGGCTCGGT CGTTCGGCTG CGCGAGCGG TATCAGCTCA CTCAAAGCG GTAATACGGT TATCCACAGA ATCAGGGGAT AACCCAGGAA AGAACATGTG  
ACGCGAGCCA GCAAGCGGAC GCCGCTGCC ATAGTCTGAGT GAGTTTCCGC CATTATGCCA ATAGTGTCT TAGTCCCTTA TTGCGTCTCT TCTTGATACAC

4401 AGCAAAAGGC CAGCAAAAGG CCAGGAACCG TAAAAAGGC CGGTTGCTGG CGTTTTCCTA TAGGCTCCGC CCCCCTGACG AGCATCACAA AAATCGACGC  
TCGTTTTCGG GTCGTTTTCG GGTCTTTGGC ATTTTTCGG CGCAACGACC GCAAAAAGGT ATCCGAGGCG GGGGACTGC TCGTAGTGT TTTAGCTGCG

4501 TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT ACCAGGCGTT TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCCGACC CTGCCGCTTA  
AGTTCAGTCT CCACCGCTTT GGGCTGTCTT GATATTCTA TGGTCCGCAA AGGGGACCT TCGAGGAGC ACGGAGAGG ACAAGGCTGG GACGGCGAAT

4601 CCGGATACCT GTCGCGCTTT CTCCTTCGG GAAGCGTGGC GCTTCTCAT AGCTCACGGT GTAGGTATCT CAGTTCGGTG TAGTCTGTTT GGTCCAAGCT  
GGCCTATGGA CAGGCGGAAA GAGGAAGCC CTTGCGACCG CGAAAGATG TCGAGTGCGA CATCCATAGA GTCAAGCCAC ATCCAGCAAG CGAGGTTTCCA

4701 GGGCTGTG CACGACCCC CGGTTTCAGC CGCTTATCCG GTAACATCG TCTTGACTCC AACCCGGTAA GACACGACTT ATGCCACTG  
CCCGACACAC GTGCTTGGG GGCAGTCCG GCTGGCGACG CGGAATAGGC CATTGATAGC AGAATCAGG TTGGGCCATT CTGTGCTGAA TAGCGGTGAC

4801 GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC TACAGAGTTC TTGAAGTGGT GGCCTAACTA CGGCTACACT AGAAGGACAG  
CGTCGTCGGT GACCAATGTC CTAATCGTCT CGCTCCATAC ATCCGCCACG ATGTCTCAG AACTTCACCA CCGGATTGAT GCCGATGTA TCTTCTCTGTC

4901 TATTGTGAT CTGCGCTCTG CTGAAGCCAG TTACCTTCGG AAAAAGAGTT GGTAAGTCTT GATCCGGCAA ACAAAACCACC GCTGGTAGCG GTGGTTTTTT  
ATAAACCATTA GACGCGAGAC GACTTCGGTC AATGGAAGCC TTTTCTCAA CCATCGAGAA CTAGGCCGTT TGTTTGGTGG CGACCATCGC CACCAAAAAA

5001 TGTTTGCAG CAGCAGATTA CGCGCAGAAA AAAAGGATCT CAAGAAGATC CTTTGATCTT TTCTACGGGG TCTGACGCTC AGTGAACGA AAATCACGT  
ACAAACGTC GTCGTCTAAT GCGCGTCTTT TTTTCTCTAGA GTTCTCTTAG GAAACTAGAA AAGATGCCCC AGACTGCCAG TCACCTTGCT TTTGAGTGCA

5101 TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCCT TTTAAATTA AAATGAAGTT TTAATCAAT CTAAGTATA TATGAGTAA  
ATTCCCTAAA ACCAGTACT TAATAGTTTT TCCTAGAAAT GGATCTAGGA AAATTTAAT TTTACTTCAA AATTAGTTA GATTTCATAT ATACTCATTT

5201 CTTGGTCTGA CAGTTTACAA TGCCTTAATCA GTGAGGCACC TATCTCAGCG ATCTGTCTAT TTCGTTTCATC CATAGTTGCC TGACTCCCCG TCGTGTAGAT  
GAACCACT GTCATGGTT ACGAATTAGT CACTCCGTGG ATAGATCGC TAGACAGATA AAGCAAGTAG GTATCAACGG ACTGAGGGGC AGCAGATCTA

**FIG.\_26F**

5301 AACTACGATA CGGGAGGGCT TACCATCTGG CCCAGTGTCT GCAATGATAC CGCGAGACCC AGGCTCACCG GCTCCAGATT TATCAGCAAT AAACCAGCCA  
TTGATGCTAT GCCCTCCCGA ATGGTAGACC GGGGTACGA CGTTACTATG GCGTCTGGG TCCGAGTGGC CGAGGTCTAA ATAGTCGTTA TTTGGTCCGT

5401 GCGGGAAGG CCGAGCGCAG AAGTGGTCTT GCAACTTTAT CCGCTCCAT CCAGTCTATT AATTGTTGCC GGAAGCTAG AGTAAGTACT TCGCCAGTTA  
CGGCTTCCC GGCTCGGTC TTCACCAGGA CGTTGAATA GCGGAGGTA GGTGAGATA TTAACAACGG CCCTTCGATC TCATTCAATCA AGCGGTCAAT

5501 ATAGTTTGG CAACGTTGTT GCCATTGCTG CAGGCATCGT GGTGTACGC TCGTGTGTTG GTATGGCTTC ATTCACTCC GGTTCCTAAC GATCAAGGCG  
TATCAAAACGC GTTGCAACAA CGGTAACGAC GTCCGTAGCA CCACAGTGG AGCAGCAAC CATAACGAAG TAAGTCGAGG CCAAGSGTTG CTAGTTCGCG

5601 AGTTACATGA TCCCCCATGT TGTGCAAAA AGCGGTTAGC TCCTTCGGTC CTCCGATCGT TGTGAGAAGT AAGTTGGCCG CAGTGTATC ACTCATGGTT  
TCAATGTACT AGGGGGTACA ACACGTTTTT TCGCCCATCG AGAAGCCAG GAGGTAGCA ACAGTCTTCA TTCAACCGGC GTCACAATAG TGAGTACCAA

5701 ATGGCAGCAC TGCATAATTC TCCTACTGTC ATGCCATCCG TAAGATGCTT TTCTGTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA TAGTGTATGC  
TACCGTCGTG ACGTATTAG AGAATGACAG TACGGTAGG AATCTACGAA AAGACACTGA CCACCTCATGA GTTGGTTTCA TAAGACTCTT ATCACATACG

5801 GCGCACCGAG TTGCTCTTGC CCGGCGTCAA CACGGGATAA TACCGGCCCA CATACAGAA CTTTAAAAGT GCTCATCATT GGAACACGTT CTTCGGGGGG  
CCGCTGGCTC AACGAGAACG GGCCGCAGTT GTGCCCTATT ATGGCGCGGT GTATCGTCTT GAAATTTTCA CGAGTAGTAA CCTTTTGCAA GAAGCCCCGC

5901 AAAACTCTCA AGGATCTTAC CGCTGTTGAG ATCCAGTTTG ATGTAACCCA CTCGTGCACC CAACGTATCT TCAGCATCTT TTACTTTTAC CAGCGTTTCT  
TTTTGAGAGT TCCTAGAATG GCGACAACTC TAGGTCAAGC TACATTGGGT GAGCACGTGG GTTGACTAGA AGTCGTAGAA AATGAAAGTG GTCGCAAGA

6001 GGGTGAGCAA AAACAGGAAG GCAAAATGCC GAATAAGGC GACACGGAAA TGTGAAATAC TCATACTCTT CCTTTTCAA TATTATTGAA  
CCCACTCGTT TTTGTCCCTC CGTTTTACGG CGTTTTTTCC CTTATTTCCC CTGTGCCCTT ACAACTTATG AGTATGAGAA GGAAAAAGTT ATAATACTT

6101 GCATTATCA GGGTTATTGT CTCATGAGCG GATACATATT TGAATGTATT TAGAAAAATA AACAAATAGG GGTTCGCGC ACATTTCCCC GAAAAAGTCCC  
CGTAAATAGT CCCAATAACA GAGTACTCGC CTATGTATAA ACTTTATATA ATCTTTTAT TTGTTTATCC CCAAGGCGCG TGTAAGGGG CTTTTACGG

6201 ACCTGACGTC TAAGAAACCA TTATTATCAT GACATTAAAC TATAAAATA GGCGTATCAC GAGGCCCTTT CGTCTTCAAT ACAGGTAGAC CTTTCGTAGA  
TGGACTGCAG ATTCTTTGGT AATAATAGTA CTGTAATGG ATATTTTTAT CCGCATAGTG CTCGCGGAAA GCAGAAAGTTA TGTCCATCTG GAAAGCATCT

6301 GATGTACAGT GAAATCCCCG AAATTATACA CATGACTGAA GGAAGGAGC TCGTCATTCC CTGCCGGGT ACCTCACCTA ACATCACTGT TACTTTAAA  
CTACATGTCA CTTTAGGGC TTTAATATGT GTACTGACTT CCTTCCCTCG AGCAGTAAGG GACGGCCCAA TGCAGTGGAT TGAGTGACA ATGAAATTTT

**FIG.\_26G**

6401 AAGTTTCCAC TTGACACTTT GATCCCTGAT GGAAGCGA TAATCTGGGA CAGTAGAAG GGCTTCATCA TATCAATGC AACGTACAAA GAAATAGGGC  
TTCAAAGGTG AACTGTGAAA CTAGGGACTA CCTTTTGGGT ATTAGACCCCT GTCATCTTTC CCGAAGTAGT ATAGTTTACG TTGCATGTTT CTTTATCCCC

6501 TTCTGACCTG TGAAGCAACA GTCATATGGG ATTTGTATAA GACAAACTAT CTCACACATC GACAAACCAA TACAATACAG GTAGACCTTT CGTAGAGATG  
AAGACTGGAC ACTTCCTGTG CAGTTACCCG TAAACATATT CTGTTTGATA GAGTGTGTAG CTGTTTGTTT ATGTTATGTC CATCTGGAAA GCATCTCTAC

6601 TACAGTGAAA TCCCCGAAAT TATACACATG ACTGAAGGAA GGGAGCTCGT CATTCCTGCG CGGGTTACGT CACCTAACAT CACTGTACT TTAATAAAGT  
ATGTCACCTT AGGGGCTTIA ATATGTGTAC TGACTTCCCT CCCTCGAGCA GTAAGGGACG GCCCAATGCA GTGGATTGTA GTGACAATGA AATTTTTC

6701 TTCCACTTGA CACTTTGATC CCTGATGGAA AACGCATAAT CTGGGACAGT AGAAGGGCT TCATCATATC AAATGCAACG TACAAGAAA TAGGGCTTCT  
AAGGTGAACT GTGAACACTAG GGACTACCTT TTCCGTATTG GACCCTGTCA TCTTCCCGA AGTAGATAG TTTACGTTGC ATGTTCTTTT ATCCCGAAGA

6801 GACCTGTGAA GCAACAGTCA ATGGGCATTT GTATAAGACA AACTATCTCA CACATCGACA AACCAATACA ATCTACAGGT AGACCTTTCG TAGAGATGTA  
CTGGACACTT CGTTGTGAGT TACCCGTAAA CATATTCTGT TTGATAGAGT GTGTAGCTGT TTGGTTATGT TAGATGTCCA TCTGGAAAGC ATCTCTACAT

6901 CAGTGAATC CCCGAAATTA TACACATGAC TGAAGGAAGG GAGCTCGTCA TTCCCTGCGG GGTACCTCA CCTAACATCA CTGTTACTTT AAAAAAGTTT  
GTCACTTTAG GGGCTTTAAT ATGTGTACTG ACTTCCCTTCC CTCGAGCAGT AAGGGACGGC CCAATGCAGT GGATTGTAGT GACAATGAAA TTTTTC

7001 CCACTTGACA CTTTGTATCCC TGATGGAAA CGCATAATCT GGGACAGTAG AAAGGGCTTC ATCATATCAA ATGCAACGTA CAAAGAAATA GGGCTTCTGA  
GGTGAAGTGT GAAACTAGGG ACTACCTTTT GCGTATTAGA CCCTGTATC TTTCCCGAAG TAGTATAGTT TACGTTGCAT GTTCTTTTAT CCGAAGACT

7101 CCTGTGAAGC AACAGTCAAT GGGCATTTGT ATAAGACAAA CTATCTCACA CATCGACAAA CCAATACAAT C  
GGACACTTCG TTGTCACTTA CCGGTAACA TATTCTGTTT GATAGAGTGT GTAGCTGTTT GGTATGTTA G

FIG.\_26H

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1  ATGAAAGA ATATCGGATT TCTTCTTGCA TCATATGTTG TTTTCTCTAT TGCTACAAAT GCCTATGAG ATATCCAGAT GACCCAGTCC CCGAGCTCCC
   TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTC TATAGTCTA CTGGTTCAGG GGCTCGAGGG
1  M K K N I A F L L A S M F V F S I A T N A Y A D I Q M T Q S P S S L
   ^met
   ^start of stII signal sequence
   ^start of light chain

101 TGTCGGCTC TGTTGGCGAT AGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTGTCCA CTGCTGTAGC CTGGTATCAA CAGAAACCAG GAAAGCTCC
   ACAGGGGAG ACACCCGCTA TCCAGTGGT AGTGGACGGC ACGGTCAGTC CTACACAGGT GACGACATCG GACCATAGTT GTCTTTGGTC CTTTTCGAGG
35  S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A P
   ^CDR-L1

201 GAAGCTTCTG ATTTACTCGG CATCCTTCTT CTACTCTGGA GTCCCTTCTC GCTTCTCTGG TAGCGGTTC GGGACGGATT TCACTCTGAC CATCAGCAGT
   CTTGGAAGAC TAAATGAGCC GTAGGAAGGA GATGAGACCT CAGGGAAGAG CGAAGAGACC ATCGCCAAGG CCCTGCCTAA AGTGAGACTG GTAGTCGTCA
68  K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S S
   ^CDR-L2

301 CTGCAGCGG AGACTTCGC AACTTATTAC TGTGAGCAAC ATTATACTAC TCCTCCACG TTCCGGACAGG GTACCAAGGT GGAGATCAA CGAACTGTGG
   GACGTCGGC TTCTGAAGCG TTGAATAATG ACAGTCGTTG TAATATGATG AGGAGGTGC AAGCCTGTCC CATGGTTCCA CCTTAGTTT GCTTGACACC
101 L Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T V A
   ^CDR-L3

401 CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAATCT GGAATGCTT GAACTGCTGCTT CCGTCTGAT AACTTCTATC CCAGAGAGGC
   GACGTGGTAG ACAGAACTAG AAGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGGA GACAACACAC GACGACTTIA TTGAAGATAG GGTCTCTCCG
135  A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A

501 CAAAGTACAG TGAAGGTGG ATACGCCCT CCATCGGCT AACTCCAGG AGAGTGTAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC
   GTTTCATGTC ACCTTCACAC TATTGCGGGA GGTAGCCCA TTGAGGGTCC TCTCACAGTG TCTCGTCTG TCGTCTCTGT CGTGGATGTC GGAGTCGTGCG
168  K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S

601 ACCCTGAGC TGAGCAAGC AGACTACGAG AAACACAAG TCTACGCCCTG CGAAGTCACC CATCAGGSCC TGAGCTGCCC CGTCACAAAG AGCTTCAACA
   TGGGACTCGG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATCGGAC GCTTCAGTGG GTAGTCCCGG ACTCGAGCGG GCAGTGTTC TCGAAGTTGT
201 T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R

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FIG.-27A



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701 GGGGAGAGTG TGGTGCCAGC TCCGGTATGG CTGATCCGAA CCGTTTCCGC GGTAAAGACC TGGCATAACT CGAGGCTGAT CCTCTACGCC GGACGCATCG
CCCCTCTCAC ACCACGGTCG AGGCCATACC GACTAGGCTT GGCAAGGCG CCATTCTCTGG ACCGTATTGA GCTCCGACTA GGAGATGGCG CCTCGGTAGC
235 G E C G A S S G M A D P N R F R G K D L A O
        ^end of light chain, start of gD tag

801 TGGCCCTAGT ACACAAGTTC ACGTAAAGAG GGTAAACAGA GGTGAGGTG ATTTATGAA AAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT
ACCGGGATCA TGCCTTCAAG TGCATTTTTC CCATTGATCT CCAACTCCAC TAAATACTT TTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA
-23      M K K N I A F L L A S M F V F
        ^start of stII

901 TCTATTGCTA CAAACGGCTA CGCTGAGGTT CAGCTGGTGG AGTCTGCGG TGGCTGGTG CAGCCAGGG GCTCACTCCG TTTGTCTCTGT GCAGCTTCTG
AGATAACGAT GTTTGGCAT GCGACTCCAA GTCGACCACC TCAGACCGCC ACCGACCAC GTCGGTCCCC CGAGTGAGG AACACAGGACA CGTCGAAGAC
-8 S I A T N A Y A E V Q L V E S G G L V Q P G G S L R L S C A A S G
        ^start of heavy chain

1001 GCTTCACCAT TAGTGGTTCT TGGATACACT GGGTGGCTCA GGCCCGGGT AAGGCCTGG AATGGGTGC TTGGATTGCT CTTATAGCG GCGTACTGA
CGAAGTGGTA ATCACCAAGA ACCTATGTA CCCACGAGT CCGGGGCCA TTCCGGACC TTACCCAACG AACCTAACGA GGAATATCG CCGCATGACT
27 F T I S G S W I H W V R Q A P G K G L E W V A W I A P Y S G A T D
        ^CDR-H2

1101 CTATGCCGAT ACGTCAAGG GCCGTTTTCAC TATAAGCSCA GACACATCCA AAAACACAGC CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC
GATACGGCTA TCGCAGTTCC CGGCAAGTG ATATTCCGCT CTGTGTAGGT TTTTGTGTCG GATGGATGTT TACTTGTCGA ATTCTCGACT CCTGTGACGG
60 Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T A

1201 GTCTATTATT GTCAAGAGA GGGGGGGTTG TACTGGGTGT TCGACTACTG GGTCAAGGA ACACTAGTCA CCGTCTCTC GGCCTCCACC AAGGGCCCAT
CAGATAATAA CACGTTCTCT CCCCCCGAAC ATGACCCACA AGCTGATGAC CCCAGTTCCT TGTGATCAGT GGCAGAGGAG CCGGAGGTGG TTCCCGGGTA
93 V Y Y C A R E G G L Y W V F D Y W G Q G T L V T V S S A S T K G P S
        ^CDR-H3

1301 CGGTCTTCCC CCTGGCACC TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT GCGTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG
GGCAGAAGG GGACCGTGG AGGAGGTTCT CGTGGAGACC CCGGTGTGCG CCGGACCCGA CGGACAGTT CCTGATGAAG GGGCTTGGCC ACTGCCACAG
127 V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V S

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FIG.\_27B

1401 GTGGAAC TCA GCGCCCTGA CCAGCGCGGT GCACACCTTC CCGGTGTCC TACAGTCCCTC AGGACTCTAC TCCCTCAGCA GCGTGGTGAC CGTGCCTCTCC  
 CACCTTGAGT CCGCGGGACT GGTGCGCGCA CGTGTGGAAG GGCCGACAGG ATGTCAGGAG TCCTGAGATG AGGAGTCGT CGCACCACCTG GCACGGGAGG  
 160 W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P S  
 1501 AGCAGCTGG GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCAG CAACACCAAG GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAACCTC  
 TCGTCGAACC CGTGGGCTG GATGTAGACG TTGCACCTAG TGTTGGGCTC CAGCTGTCT TTCAACTCGG GTTTAGAACA CTCTTTTGAG  
 193 S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T H  
 1601 ACCTCAGTG CGTGCTCTT GGTTCGGTG ATTTGATTA TGAAGAATG GCAAACGCTA ATAAGGGGGC TATGACCGAA AATGCCGATG AAAACGGCT  
 TGGAGTCACC GCCACCGAGA CCAAGGCCAC TAAACTAAT ACTTTCTTAC CGTTTGGCAT TATCCCGCG ATACTGGCTT TTACGGCTAC TTTTGGCGGA  
 227 L S G G S G S G D F D Y E K M A N A N K G A M T E N A D E N A L  
 ^end of heavy chain  
 ^start of gene III coat protein (267-end)  
 1701 ACAGTCTGAC GCTAAAGGCA AACTTGATTC TGTCGCTACT GATTACGGTG CTGCTATCGA TGGTTTCATT GGTGAGCTTT CCGGCTTGC TAATGGTAAT  
 TGTGAGACTG CGATTTCCGT TTGAACTAAG ACAGCGATGA CTAATGCCAC GACGATAGCT ACCAAAGTAA CCACCTGCAA GGCCGGAACG ATTACCATTA  
 260 Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L A N G N  
 1801 GGTGCTACTG GTGATTTGC TGGCTCTAAT TCCCAAATGG CTCAAGTCGG TGACGGTGAT AATTCACCTT TAATGAATAA TTTCCGTCAA TATTACCTT  
 CCACGATGAC CACTAAACG ACCGAGATTA AGGTTTACC GAGTTCAGCC ACTGCCACTA TTAAGTGGA AATTACTATT AAAGCAGTT ATAATGGAA  
 293 G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q Y L P S  
 1901 CCCTCCCTCA ATCGGTTGAA TGTGCGCCTT TTGCTTTTAG CGTGGTAAA CCATATGAAT TTTCTATTGA TTGTGACAAA ATAACTTAT TCCGTGGTGT  
 GGGAGGGAGT TAGCCACTT ACAGCGGAA AACAGAAATC GCGACCATTT GGTATACCTA AAAGATAACT AACACTGTTT TATTGAATA AGGCACCACA  
 327 L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N L F R G V  
 2001 CTTTGGCTT CTTTATATG TTGCCACCTT TATGTATGA TTTTCTACGT TTGCTAACAT ACTGCGTAAT AAGAGTCTT AA  
 GAAACGCAA GAAATATAC AACGGTGGAA ATACATACAT AAAAGATGCA AACGATTGTA TGACGCTATA TTCTCAGAA TT  
 360 F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

**FIG. 27C**

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1  ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTGG TTTTCTCTAT TGCTACAAAT GCCTATGCAG ATATCCAGAT GACCCAGTCC CCGAGCTCCC
   TACTTTTCT TATAGCGTAA AGAAGACGT AGATACAAGC AAAAAGATA ACATGTTTA CGGATACGTC TATAGTCTTA CTGGTCAGG GGCTCGAGGG
1M  K K N I A F L L A S M F V F S I A T N A Y A D I Q M T Q S P S S L
   ^met
   ^start of stII signal sequence

101 TGTCGGCTC TGTGGCGAT AGGTCACCA TCACCTGCCG TGCAGTCAG GATGTGTCCA CTGCTGTAGC CTGGTATCAA CAGAAACCAG GAAAAGTCC
   ACAGGGGAG ACACCCGTA TCCCAGTGGT AGTGACGGC ACGTCAGTC CTACACAGGT GACGACATCG GACCATAGTT GTCTTTGGTC CTTTTCGAGG
35  S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A P
   ^CDR-L1

201 GAAGCTTCTG ATTTACTCG CATCCTTCT CTACTCTGGA GTCCTTCTC GCTTCTCTGG TAGCGGTTCC GGGACGGATT TCACCTCTGAC CATCAGCAGT
   CTTGGAAGAC TAAATGAGC GTAGGAAGCA GATGAGACCT CAGGAAGAG CGAAGAGACC ATCGCCAAGG CCCTGCCCTAA AGTGAGACTG GTAGTCGTCA
68  K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S S
   ^CDR-L2

301 CTGCAGCCG AAGACTTCG AACTTATTAC TGTACCAAC ATTATACTAC TCCTCCCACG TTCGGACAGG GTACCAAGT GGAGATCAAA CGAACTGTGG
   GACGTCGGC TTCTGAAGG TTGAATAATG ACAGTCGTTG TAAATGATG AGAGGGTGC AAGCCTGTCC CATGGTTCCA CCTCTAGTTT GCTTGACACC
101 L Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T V A
   ^CDR-L3

401 CTGCACCATC TGTCTTCATC TTCCCGCAT CTGATGAGCA GTTGAATCT GGAATGCCCT CTGTTGTGTG CCGTCTGAAT AACCTCTATC CCAGAGAGGC
   GACGTGGTAG ACAGAAGTAG AAGGGCGTA GACTACTCGT CAACTTTAGA CTTGACGGA GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG
135  A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A

501 CAAAGTACAG TGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG AGAGTGTAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC
   GTTTCATGTC ACCTTCCACC TATTGCGGA GGTGAGCCCA TTGAGGGTCC TCTCACAGTG TCTCGTCCCTG TCGTTCCCTGT CGTGGATGTC GGAGTCGTCG
168  K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S

601 ACCCTGAGC TGAGCAAGC AGACTACGAG AAACACAAAG TCTACGCCCTG CCAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAG AGCTTCAACA
   TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATCGCGAC GCTTCAGTGG GTAGTCCCGG ACTCGAGCGG GCAGTGTTC TCGAAGTTGT
201 T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R

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**FIG.\_28A**

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701 GGGGAGAGTG TGGTCCAGC TCCGGTATGG CTGATCCGAA CCGTTTCCGC GGTAGGACC TGGCATAACT CGAGGCTGAT CCTCTAGCC GGACGCATCG
    CCCCTCTCAC ACCACGGTCG AGCCCATACC GACTAGGCTT GGCAAAGCGG CCATTCTCTGG ACCGTATTGA GCTCCGACTA GGAGATGGG CCTGCGTAGC
235 G E C G A S S G M A D P N R F R G K D L A O
    ^end of light chain, start of gD tag

801 TGGCCCTAGT ACCGAAGTTC ACGTAAAAG GGTAACTAGA GGTGAGGTG ATTTTATGAA AAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT
    ACCGGGATCA TGGGTTCAAG TGCATTTTTC CCATTGATCT CCAACTCCAC TAAATACTTT TTCTTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAA
    M K K N I A F L L A S M F V F
    ^start of stII

-23

901 TCTATTGCTA CAAACGGGTA CGCTGAGGTT CAGCTGGTGG AGTCTGGGG TGGCCTGGTG CAGCAGGGG GCTCACTCCG TTGTCTCTGT GCAGCTTCTG
    AGATAACGAT GTTGGGCAT GCGACTCCAA GTCGACCACC TCAGACCGCC ACCGACCCAC GTGGGTCCCC CGAGTGAGGC AACACAGGACA CGTCGAAGAC
-8 S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R L S C A A S G
    ^start of heavy chain

1001 GCTTCACCAT TAGTAATTAT GGGATACACT GGGTGGCTCA GGCCCGGGT AAGGCCTGG AATGGGTGG TAGGATTCTT CCTTCTAACG GCTCTACTTA
    CGAAGTGGTA ATCATTATA CCTATGTGA CCCACGGAGT CCGGGGCCCA TTCCGGGACC TTACCCAAACC ATCCTAAAGA GGAAGATTGC CGAGATGAAT
27 F T I S N Y G I H W V R Q A P G K G L E W V G R I S P S N G S T Y
    ^CDR-H2

1101 CTATGCCGAT AGGTCAGG GCGTTTTCAC TATAAGCGCA GACACATCCA AAAACACAGC CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC
    GATACGGCTA TCGCAGTTCC CGGCAAAGTG ATATTCCGGT CTGTGTAGGT TTTTGTGTCTG GATGGATGTT TACTTGTCGA ATTCTCGACT CCTGTGACGG
60 Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T A

1201 GTCTATTATT GTCAAAATG CTCGGTCAGG TTCGCTTACT GGGTCAAGG AACACTAGTC ACCGTCTCCT CGGCCTCCAC CAAGGGCCCA TCGGTCTTCC
    CAGATAATAA CACGTTTTAC GAGCCAGTCC AAGCGAATGA CCCCAGTTCC TTGTGATCAG TGGCAGAGGA GCCGGAGGTG GTTCCCGGCT AGCCAGAAGG
93 V Y Y C A K C S V R F A Y W G Q G T L V T V S S A S T K G P S V F P
    ^CDR-H3

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FIG.\_28B

1301 CCCTGGCACC CTCCTCCRAAG AGCACTCTG GGGGCACAGC GGCCTGGGC TGCCTGGTCA AGGACTACTT CCCCAGACCG GTGACGGTGT CGTGGAACTC  
 GGGACCGTGG GAGGAGGTTT TCGTGGAGAC CCCCCTGTTC CCGGACCCG ACGGACCACT TCCTGATGAA GGGCTTGGC CACTGCCACA GCACCTTGAG  
 127 L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V S W N S  
 1401 AGCGGCCCTG ACCAGCGGGG TGCACACACTT CCCGGCTGTC CTACAGTCTC CAGGACTCTA CTCCTCAGC AGCGTGGA CCGTGCCCTC CAGCAGCTTG  
 TCCGGGGAC TGGTCGCCG CCGTGTGGAA GGGCCGACAG GATCTCAGGA GTCCTGAGAT GAGGAGTCG TCGCACCACT GGCACGGGAG GTCGTCAAC  
 160 G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P S S S L  
 1501 GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCACACCAA GGTGCAAG AAGTTGAGC CCAATCTTG TGACAAAAC CACCTCAGT  
 CCGTGGGTCT GGATGTAGAC GTTGCACTTA GTGTTGGGT CCGTTGGGT CCAGCTGTC TTTCARCTCG GGTTTAGAAC ACTGTTTGA GTGAGTCACT  
 193 G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T H L S G  
 start of gene III coat protein (267-end)  
 1601 GCGTGGCTC TGGTCCGGT GATTTTGATT ATGAAAAGAT GGCACACGCT AATAAGGGG CTATGACCGA AAATGCCGAT GAAAACGGC TACAGTCTGA  
 CGCCACCGAG ACCAAGGCA CTAAACTAA TACTTTTCTA CCGTTGCGA TTATTCCTCC GATCTGGCT TTACGCGCTA CTTTGGCGG ATGTCAGACT  
 227 G G S G S G D F D Y E K M A N A N K G A M T E N A D E N A L Q S D  
 1701 CGCTAAAGC AACTTGATT CTGTCGCTAC TGATTACGGT GCTGCTATCG ATGGTTTCAT TGGTGACGTT TCCGGCCTTG CTAATGGTAA TGGTGTCTACT  
 GCGATTTCCG TTTGAACATA GACAGCGATG ACTAATGCCA CGACGATAGC TACCAAGTA ACCACTGCAA AGGCCGGAAC GATTACCAAT ACCACGATGA  
 260 A K G K L D S V A T D Y G A A I D G F I G D V S G L A N G N G A T  
 1801 GGTGATTTTG CTGGCTCTAA TTCCCAATG GCTCAAGTCG GTCAAGTCG TAATTCACCT TTAATGAATA ATTTCCGTC AATTTACCT TCCCTCCCTC  
 CCACTAAAC GACCGAGATT AAGGTTTAC CAGTTTCAGC CACTGCCACT ATTAAGTGA AATTACTTAT TAAAGGCAGT TATAAATGA AGGAGGGAG  
 293 G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q Y L P S L P Q  
 1901 AATCGTTGA ATGTCGCCCT TTTGTCTTTA GCGCTGGTAA ACCAATGAA TTTTCTATTG ATTGACAA AATAAACCTA TTCCGTGGTG TCTTTGCGTT  
 TTAGCCAACT TACAGCGGGA AACAGAAAT CCGGACCAAT TGGTATACTT AAAAGATAAC TAACACTGTT TTATTTGAT AAGGCACCAC AGAAACGCAA  
 327 S V E C R P F V F S A G K P Y E F S I D C D K I N L F R G V F A F  
 2001 TCTTTTATAT GTTGCACCT TTATGTATGT ATTTCTACG TTTGCTAACA TACTGCGTAA TAAGAGTCT TAA  
 AGAAATATA CACGGTGA AATACATACA TAAAGATGC AAACGATGT ATGACGCAAT ATTCCTCAGA ATT  
 360 L L Y V A T F M Y V F S T F A N I L R N K E S O

FIG.-28C

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1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAT GCCTATGCAT CCGATATCCA GATGACCCAG TCCCCGAGCT
TACTTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTA GGCTATAGGT CTACTGGGTC AGGGGCTCGA
1 M K K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S
^met
^start of stII signal sequence
^light chain start

101 CCCTGTCCGC CTCTGTGGC GATAGGGTCA CCATCACCTG CCCTGCCAGT CAGGATGTGT CCACTGCTGT AGCCTGGPAT CAACAGAAAC CAGGAAAAGC
GGGACAGGCG GAGACACCGG CTATCCAGT GGTAGTGGAC GGCACGGTCA GTCCTACACA GGTGACGACA TCGGACCATA GTTGTCTTTG GTCCTTTTCG
35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A
^CDR-L1

201 TCCGAAGCTT CTGATTACT CGGATTCCTT CCTCTACTCT GGAGTCCCTT CTGGCTTCTC TGGTAGCGGT TCCGGGACGG ATTTCACTCT GACCATCAGC
AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGATGAGA CCTCAGGGAA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG
68 P K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S
^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTCTCAGC AATCTTATAC TACTCTCCCTCC AGGTTCCGAC AGGTTACCAA GGTGGAGATC AAACGAAGTC
TCAGACGTCG GCCTTCTGAA CGGTTGAATA ATGACAGTCG TTAGAATATG ATGAGGAGGG TGCAAGCCTG TCCCATGTTT CCACCTCTAG TTTTGTGTGAC
101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V
^CDR-L3

401 TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA TCTGGAACCTG CCTCTGTTGT GTGCCTGCTG AATACTTCT ATCCAGAGA
ACCGACGTGG TAGACAGNAG TAGAAGGCGG GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATTGAAGA TAGGCTCTCT
135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E

501 GGCCAAAGTA CAGTGGAGG TGGATAACGC CCTCCAATCG GGTAACTCCC AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
CCGGTTTCTAT GTCACCTTCC ACCTATTCCG GGAGGTAGC CCATTGAGG TCCTCTCACA GTGTCTCGTC CTGTCTGTTCC TGTCGTGGAT GTCCGAGTCCG
168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S

601 AGCACCCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCCATCAGG GCCTGAGTCT GCCCGTCACA AAGAGCTTCA
TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCCTTGTGT TTGAGATCGG GAGCTTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT
201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

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FIG.\_29A

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701 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGGCTGATCC GAACCGTTTC CGGGTAAGG ACCTGGCATA ACTCGAGGCT GATCCTCTAC GCCGGACGCA  
TGTCCTCTCT CACACCACGG TCGAGGCCAT ACCGACTAGG CTTGGCAAG GGGCCATTCC TGGACCGTAT TGAGCTCCGA CTAGGAGATG CGGCCTGCGT  
235 R G E C G A S S G M A D P N R F R G K D L A O  
^end of light chain, start of gD tag

801 TCGTGGCCCT AGTACGGAAG TTCACGTAAG AAGGTAACCT AGAGGTGAG GTGATTTTAT GAAAAAGAAAT ATCGCATTTT TTTCTGCATC TATGTTTCGT  
AGCACCGGGA TCATGCGGTT CAGTGCATTT TTCCCATTTGA TCTCCAACTC CACTAAAATA CTTTTTCTTA TAGCGTAAG AAGAACGTAG ATACAAGCAA  
-23 M K K N I A F L L A S M F V  
^start of stII

901 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCACCTGG TGAGTCTGG CGGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT  
AAAAGATAAC GATGTTTGGG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CACGTCGGTC CCCCAGATGA GGCAACACAGG ACACGTCGAA  
-9 F S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R L S C A A S  
^start of heavy chain ^CDR-H1

1001 CTGGCTTAC CATTAGTGGT TCTGATATAC ACTGGTGCG TCAGGCCCGG GGTAAAGGCC TGAATGGGT TGGTAGGATT TCTCCTTATG GCGCAATAC  
GACCGAAGTG GTAATCACCA AGACTATATG TGACCACGC AGTCGGGGC CCATTCGCG ACCTTACCA ACCATCTTAA AGAGGAATAC CGCGTTATG  
26 G F T I S G S D I H W V R Q A P G K G L E W V G R I S P Y G G N T  
^CDR-H2

1101 TAACTATGCC GATAGCGTCA AGGCCCGTTT CACTATAAGC GCACACACAT CCAAAAACAC AGCTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT  
ATTGATACGG CTATCGCAGT TCCCGGCATA GTGATATTCTG CGTCTGTGTA GGTTTTGTG TCGGATGGAT GTTTACTTGT CGAATTCTCG ACTCCTGTGA  
59 N Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T

1201 GCGTCTATT ATTGTGCAAG AGTCGGCGGC CTCAAGTTGC TGTTCTGACTA CTGGGGTCAA GGAACACTAG TCACCGTCTC CTCGGCTCC ACCAAGGGCC  
CGGCAGATAA TAACACGTTT TCAGCCCGCG GAGTTCAACG ACAAGCTGAT GACCCAGTT CTTGTGTATC AGTGGCAGAG GAGCCGGAGG TGGTTCCCGG  
92 A V Y Y C A R V G G L K L L F D Y W G Q G T L V T V S S A S T K G P  
^CDR-H3

1301 CATCGGTCTT CCCCCTGGCA CCTCTCTCCA AGAGCACTC TGGGGGCACA GGGGCCCTGG GCTGCCTGGT CAAGGACTAC TTCCCCGAAC CGGTGACGGT  
GTAGCCAGAA GGGGGACCGT GGGAGGAGT TCTCGTGGAG ACCCCGCTGT CCGCGGAC CGACGGACCA GTTCTGTATG AAGGGGCTTG GCCACTGCCA  
126 S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V

FIG.\_29B

1401 GTCGTGAAC TCAGGCGCC TGACGACCG CGTGACACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGCGTGGT GACCGTGCCC  
 CAGCACCTTG AGTCGCGGG ACTGTCGCC GCACGTGTGG AAGGGCCGAC AGGATGTGAG GAGTCCTGAG ATGAGGAGT CGTGCACCA CTGGCACGGG  
 159 S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P  
 1501 TCCAGGAGCT TGGGCACCCA GACCTACATC TGAACGTGA ATCACAAGCC CAGCAACACC AAGGTCGACA AGAAGTTGA GCCAAATCT TGTGACAAAA  
 AGGTGCTCGA ACCCGTGGT CTGGATGTAG ACCTTGCACT TAGTGTTCGG GTCGTTGTTGG TTCCAGTGT TCTTTCAACT CGGTTTGA ACACGTGTTT  
 192 S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T  
 1601 CTCACGGCG CATGAACAG CTAGAGGACA AGTCGAAGA GCTACTCTCC AAGAATACC ACCTAGAGAA TGAAGTGGCA AGACTCAAAA AACTGTGCGG  
 GAGTGCGGC GTACTTGTG GATCTCTGT TCCAGCTTCT CGATGAGAGG TTCTTGATGG TGGATCTCTT ACTTCACCGT TCTGAGTTT TTGAACAGCC  
 226 H G R M K Q L E D K V E E L L S K N Y H L E N E V A R L K K L V G  
 'end of heavy chain, start of leucine zipper  
 1701 GGAGCGCGA AAGCTTAGTG CGGTGGCTC TGTTCCGGT GATTTTGATT ATGAAAAGAT GGCAACGCT AATAAGGGG CTATGACCGA AAATGCCGAT  
 CCTCGGCCCT TTCGATCAC CGCCACCGAG ACCAAGGCCA CTAAACTTAA TACTTTTCTA CCGTTTCCGA TTATTTCCCC GATACTGGCT TTACGGCTA  
 259 E R G K L S G G S G D F D Y E K M A N A N K G A M T E N A D  
 'end of leucine zipper, gene III coat protein (267-end)  
 1801 GAAAACGCG TACAGTCTGA CGCTAAAGGC AAACCTTGATT CTGTGCTAC TGATTACGGT GCTGCTATCG ATGTTTTCAT TGGTGACGTT TCCGGCCTTG  
 CTTTTCGGG ATGTCAGACT GCGATTTCG TTTCGAACCTA GACAGCGATG ACTAATGCCA CGACGATAGC TACCAAAGTA ACCACTGCAA AGGCCGGAAC  
 292 E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L A  
 1901 CTAATGTAA TGGTGCTACT GGTGATTTTG CTGCTCTAA TTCCCAAATG GCTCAAGTCG GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCCGTCA  
 GATTACCAT ACCACGATGA CCACATAAAC GACCGAGATT AAGGTTTAC CGAGTTCAGC CACTGCCACT ATTAAGTGA AATTACTTAT TAAAGGCAGT  
 326 N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q  
 2001 ATATTACCT TCCCTCCCTC AATCGGTTGA ATGCGCCCT TTGTCTTTA GCGTGGTAA ACCATATGAA TTTTCTATG ATTGTGACAA AATAAACTTA  
 TATAATGGA AGGAGGGAG TTAGCCAAC TACAGCGGA AACAGAAAT CGCGACCAAT TGGTATACTT AAAAGATAAC TAACACTGTT TTATTTGAAT  
 359 Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N L  
 2101 TTCCGTGGT TCTTTGCTT TCTTTTATAT GTTGCACCT TTATGTATGT ATTTTCTACG TTGCTAACA TACTGCGTAA TAAGGAGTCT TAA  
 AAGGCACCAC AGAAACGCA AGAAATATA CAACGGTGA AATACATACA TAAAGATGC AAACGATTGT ATGACGCAAT ATTCCTCAGA ATT  
 392 F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

**FIG.\_29C**



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1 ATGAAAAGA ATATCGCATT TCTTCTTCCA TCTATGTTCC TTTTCTTCTAT TGCTACAAAT GCCTATGCAAT CCGATATCCA GATGACCCAG TCCCCGAGCT
TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACATGTTTA CGGATACGTA GGCTATAGGT CTACTGGGTC AGGGGCTCGA
1 M K K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S
^start of stII signal sequence
^met
^light chain start

101 CCCTGTCCGC CTCTGTGGC GATAGGGTCA CCATCACCTG CCGTGCCAGT CAGGATGTGT CCACTGCTGT AGCCTGGTAT CAACAGAAAC CAGGAAAAGC
GGGACAGGCG GAGACACCCG CTATCCCACT GGTAGTGGAC GGCACGGTCA GTCCTACACA GTGACGACA TCGGACCATA GTTGCTTTTG GTCCTTTTCG
35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A
^CDR-L1

201 TCCGAAGCTT CTGATTACT CGGCATCCTT CCTCTACTCT GGAGTCCCTT CTCGCTTCTC TGGTAGCGGT TCCGGGACGG ATTTCACTCT GACCATCAGC
AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGATGAGA CCTCAGGGAA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG
68 P K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S
^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTGAGC AATCTTATAC TACTCTCTCC ACCTTCGGAC AGGTACCAA GGTGGAGATC AAACGAACTG
TCAGACGTCG GCCTTCTGAA CGGTTGAATA ATGACAGTCG TTAGATATAG ATGAGGAGGG TGAAGCCTG TCCCATGGTT CCACCTCTAG TTTCGCTTGAC
101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V
^CDR-L3

401 TGCTGCACC ATCTGTCTTC ATCTTCCGC CATCTGATGA GCAGTTGAAA TCTGGAACCTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA
ACCGACGTCG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATTGAAGA TAGGGTCTCT
135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E

501 GGCCAAAGTA CAGTGAAGG TGGATAACGC CCTCCAAATCG GGTAACTCCC AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
CCGGTTTCAT GTCACCTTCC ACCTATTGGG GGAGGTTAGC CCATTGAGGG TCCTCTCACA GTGTCTCGTC CTGTCTGTTCC TGTCGTGGAT GTCGGAGTCG
168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S

601 AGCACCCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
TCGTGGGACT CGGACTCGTT TCGTCTGATG CTCCTTTGTT GTTCAATGCG GACGTTTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT
201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

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FIG.\_30A

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701 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGGCTGATCC GAACGGTTTC CGCGTAAGG ACCTGGCATA ACTCGAGGCT GATCCTCTAC GCGGAGGCA
TGTCCCTCT CACACCACGG TCGAGGCCAT ACCGACTAGG CTTGGCAAAG GCGCATTC TGGACCGTAT TGAGCTCCGA CTAGGAGATG CGGCTGCGT
235 R G E C G A S S G M A D P N R F R G K D L A O
^end of light chain, start of gD tag

801 TCGTGGCCCT AGTACGCAAG TTCACGTAAA AAGGTAAC AGAGGTGAG GTGATTTTAT GAAAAAGAAT ATCGCATTC TTCTTGCATC TATGTTGTT
AGCACCGGA TCATGCGTTC AAGTGCATT TTCCCATTTA TCCTCAACTC CACTAAATA CTTTTCTTA TAGCGTAAAG AAGAACCCTAG ATACAGCAA
-23 M K K N I A F L L A S M F V
^start of stII

901 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGTGG TGGAGTCTGG CCGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGAGCTT
AAAAGATAAC GATGTTTGG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CACGTGGTC CCCGAGTGA GGCAACAGG ACACGTCGAA
-9 F S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R L S C A A S
^start of heavy chain ^CDR-H1

1001 CTGGCTTCAC CATTAATA TCCGATATAC ACTGGTGGC TCAGGCCCGG GGTAAAGGCC TGGAATGGGT TGCTACTATT TATCCTTTATG GCGGCTATAC
GACCGAAGTG GTAATGATTA AGGCTATATG TGACCCACGC AGTCGGGGC CCATTCCCGG ACCTTACCCA ACATGATATA ATAGGATATC CGCCGATATG
26 G F T I T N S D I H W V R Q A P G K G L E W V A T I Y P Y G G Y T
^CDR-H2

1101 TTACTATGCC GATAGCGTCA AGGCCCGTTT CACTATAAGC GCAGACACAT CCAAAAACAC AGCTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT
AATGATACGG CTATCGCAGT TCCCGGCCAA GTGATATTCG CGTCTGTGTA GGTTTTGTG TCGGATGGAT GTTTACTTGT CGAATTCCTG ACTCCTGTGA
59 Y Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T

1201 GCGGCTATT ATTGTGCAAG AGGGGGCGG ATGGACGGCT ACGTTATGGA CTACTGGGT CAAGGAACAC TAGTCACCGT CTCCTCGGCC TCCACCAAGG
CGGAGATAA TAACACGTTT TCCCCCGCCC TACCTGCCGA TGCAATACCT GATGACCCCA GTTCCTTGTG ATCAGTGGCA GAGGAGCCGG AGGTGTTCC
92 A V Y Y C A R G G G M D G Y V M D Y W G Q G T L V T V S S A S T K G
^CDR-H3

1301 GCCCATCGT CTTCCCCCTG GCACCTCTCT CCAAGAGCAC CTCGGGGGGC ACAGCGGCC TGGGCTGCCT GGTCAAGGAC TACTTCCCGG AACCGGTGAC
CGGGTAGCCA GAAGGGGGAC CGTGGGAGGA GGTCTCTGTG GAGACCCCGG TGTGCGCCGG ACCCGACGGA CCAGTTCTCTG ATGAAGGGC TTGGCCACTG
126 P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T

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**FIG.\_30B**

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1401 GGTGTCCTGG AACTCAGCG CGCGGTGCAC ACCTTCCCG CTGTCTCTACA GTCTACTCCC TCAGCAGCGT GGTGACCCGTG
    CCACAGCACC TTGAGTCCGC GGGACTGGTC GCCGCACGTG TGAAGGGCC GACAGGATCT CAGGAGTCTT GAGATGAGGG AGTCGTCGCA CCACTGGCAC
159 V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V

1501 CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ATCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGCTCG ACAAGAAAGT TGAGCCCAAA TCTTGTGACA
    GGGAGGTCGT CGAACCCGTG GGTCTGGATG TAGACGTTGC ACTTAGTGT CCGGTCTGTG TGGTTCAGC TGTTCTTTCA ACTCGGGTTT AGAACACTGT
192 P S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K

1601 AAACACACGG CCGCATGAAA CAGCTAGAGG ACAAGGTGCA AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGTG GCAAGACTCA AAAAACTTGT
    TTTGAGTGCC GGGGTACTTT GTCGATCTCC TGTCCAGCT TCTCGATGAG AGGTTCTTGA TGGTGGATCT CTTACTTCAC CGTTCTGAGT TTTTGAACA
226 T H G R M K Q L E D K V E E L L S K N Y H L E N E V A R L K K L V
    ^end of heavy chain, start of leucine zipper

1701 CGGGGAGCGC GGAAGCTTA GTGGGGTGG CTCTGGTTCC GGTGATTTTG ATTATGAAA GATGGCAAA GCTAATAAGG GGGCTATGAC CGAAAATGCC
    GCCCCTCGCG CCTTTCGAAT CACGCCACC GAGACCAAGG CCACATAAAC TAATACTTTT CTACCGTTTG CGATTATTC CCGATATCTG GCTTTTACGG
259 G E R G K L S G G S G S G D F D Y E K M A N A N K G A M T E N A
    ^end of leucine zipper, start of gene III coat protein (267-end)

1801 GATGAAAACG CGCTACAGTC TGACGCTAAA GGCAAACTTG ATTCTGTCC TACTGATTAC GGTGCTGCTA TCGATGGTTT CATTTGGTAC GTTCCGGGCC
    CTACTTTTGC GCGATGTCAG ACTCGGATTT CCGTTTGAAC TAAGACAGCG ATGACTAATG CCACGACGAT AGCTACCAA GTAACCACTG CAAAGGCCGG
292 D E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L

1901 TTGCTAATGG TAATGGTGCT ACTGGTGATT TTGCTGGCTC TAATCCCAA ATGGCTCAAG TCGGTGACGG TGATAATTCA CCTTAATGA ATAATTTCCG
    AACGATTACC ATTACCACGA TGACCACTAA AACGACCGAG ATTAAGGTTT TACCGAGTTC AGCCACTGCC ACTATTAAAGT GGAATTAAT TATTAAAGGC
326 A N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R

2001 TCAATATTTA CCTTCCCTCC CTCATTCGGT TGAATGTCC CCTTTTGTCT TTAGCGCTGG TAAACCATAT GAATTTTCTA TTGATTGTGA CAAATAAAC
    AGTTATAAAT GGAAGGAGG GAGTTAGCCA ACTTACAGCG GGAAACAGA AATCGCGACC ATTTGGTATA CTTAAAAGAT AACTAACACT GTTTATTGTG
359 Q Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N

2101 TTATTCGGTG GTGTCCTTTC GTTCTTTTTA TATGTTGCCA CCTTTATGTA TGTATTTTCT ACGTTTGCTA ACATAGTGG TAATAAGGAG TCTTAA
    AATAAGGCAC CACAGAAACG CAAAGAAAAT ATACAACGGT GGAATAACAT ACATAAAGA TGCAAAAGAT TGTATGACGC ATTATTCCTC AGAATT
392 L F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

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**FIG.\_30C**

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1 ATGAAAAAGA ATATCGCAFT TCTTCTTGCA TCTATGTCG TTTTCTCTAT TGCTACAAAT GCCTATGCAAT CCGATATCCA GATGACCCAG TCCCCGAGCT
TACTTTTTCT TATAGCGTAA AGAAGAAGC AGATAAAGC AAAAAGATA ACGATGTTA CCGATACGTA GGCTATAGST CTACTGGGTC AGGGCTCGA
1 M K K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S
^met ^light chain start

101 CCCTGTCCGC CTCTGTGGC GATAGGTCA CCATCACCTG CCGTGCCAGT CAGATGTGT CCACTGCTGT AGCCTGGTAT CAACAGAAAC CAGGAAAAGC
GGGACAGGGC GAGACACCCG CTATCCAGT GGTAGTGGAC GGCACGGTCA GTCTACACA GGTACGACA TCGGACCATA GTTGTCTTTG GTCCCTTTTCG
35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A
^CDR-L1

201 TCCGAAGCTT CTGATTACT CGGCATCCTT CCTCTACTCT GGAGTCCCTT CTGCTTCTC TGGTAGCGGT TCCGGGACGG ATTTCACCTCT GACCATCAGC
AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGATGAGA CCTCAGGGAA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG
68 P K L L I Y S A S F L Y S G V P S R F S G S G T D F T L T I S
^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTGAGC AATCTTATAC TACTCCTCCC AGCTTCGGAC AGGTACCAC GGTGGAGATC AAACGAACTG
TCAGACGTCG GCCTTCTGAA CGGTGGAATA ATGACACTCG TTAGATATG ATGAGGAGG TGAAGCCTG TCCCATGGTT CCACCTCTAG TTTGCTTGAC
101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V
^CDR-L3

401 TGCTGCACC ATCTGTCTTC ATCTTCCGC CATCTGATGA GCAGTTGAAA TCTGGAAGTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA
ACCGACGTCG TAGACAGAAG TAGAAGGGC GTAGACTACT CGTCACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATTGAAGA TAGGCTCTCT
135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E

501 GGCCAAAGTA CAGTGAAGG TGGATAACG CCTCCAATCG GGTAACTCCC AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
CCGTTTTCAT GTCACCTTCC ACCTATTGG GAGGTTAGC CCATTGAGG TCTCTCACA GTGTCTGTC CTGTCTGTTCC TGTCGTGGAT GTCGGAGTCG
168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S

601 AGCACCCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCTTTGTTGT TTCAGATCGG GACGTTTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT
201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

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FIG.\_31A

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701 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGGCTGATCC GAACCGTTTC CCGGGTAAGG ACCTGGCATA ACTCGAGGCT GATCCTCTAC GCCGGACGCA
    TGTCCCTCTT CACACCACGG TCGAGGCCAT ACCGACTAGG CTGCGCAAAG GGCCTATTCC TGGACCGTAT TGAGCTCCGA CTAGGAGATG CGGCCCTGCGT
235 R G E C G A S S G M A D P N R F R G K D L A O
    ^end of light chain, start of gD tag

801 TCGTGGCCCT AGTACGCAAG TTCACGTAAA AAGGTAACCT AGAGTTGAG GTGATTTTAT GAAAAAGAAT ATCGCATTTT TTCTTGCATC TATGTTGCTT
    AGCACCGGGA TCATGGGTTT AAGTGCATTT TTCCCATTTGA TCCTCAACTC CACTAAATA CTTTTCTTTA TAGCGTAAAG AAGAACCTAG ATACAGCAA
    M K K N I A F L L A S M F V
-23 ^start of stII

901 TTTTCTATTG CTACAAACGC GTACGCTCAG GTTCAGCTGG TGGAGTCTGG CCGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT
    AAAAGATAAC GATGTTTGG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CACGTGCGTC CCCCGAGTGA GGCAACAGG ACACGTGCGAA
-9 F S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R L S C A A S
    ^start of heavy chain ^CDR-H1

1001 CTGGCTTCAC CATTATAAT TATGATATAC ACTGGTGCGG TCAGGCCCGG GGTAAAGGCC TGAATGGGT TGGTTATATT TCTCTCTCTA GCGGCGCTAC
    GACCGAAGTG GTAATTATTA ATACTATATG TGACCCACGC AGTCGGGGG CATTCCCGG ACCTTACCCA ACCAATATAA AGAGGAGGAT CGCCGCGGATG
26 G F T I N N Y D I H W V R Q A P G K G L E W V G Y I S P P S G A T
    ^CDR-H2

1101 TTTACTATGCC GATAGCGTCA AGGGCCGTTT CACTATAAAGC GCAGACACAT CCAAAAACAC AGCTTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT
    AATGATACGG CTATCGCAGT TCCCGGCAAA GTGATATTGG CGTCTGTGTA GGTTTTGTG TCGGATGGAT GTTTACTTGT CGAATTCCTG ACTCCTCTGA
59 Y Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T

1201 GCCGTCTATT ATTGTGCAAG AATGGTCGGC ATGGCGAGGG GGGTTATGGA CTACTGGGGT CAAGGAACAC TAGTCACCGT CTCCTCGGCC TCCACCAAGG
    CGGCAGATAA TAACACGTTT TTACCAGCGG TACGCCCTCCC CCCAATACCT GATGACCCCA GTTCCTTGTG ATCAGTGGCA GAGGAGCCGG AGGTGGTTC
92 A V Y Y C A R M V G M R R G V M D Y W G Q G T L V T V S S A S T K G
    ^CDR-H3

1301 GCCCATCGGT CTTCCTCCCTG GCACCTCTCT CCAAGAGCAC CTCTGGGGG ACAGCGGCC TGGGCTGCCT GGTCAAGGAC TACTTCCCGG AACCGGTGAC
    CGGGTAGCCA GAAGGGGGAC CGTGGGAGGA GGTTCTCTGT GAGACCCCGG TGTCGCCCGG ACCCGACGGA CCAGTTCTCTG ATGAAGGGGC TTGGCCACTG
126 P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T

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FIG.\_31B

1401 GGTGTCGTGG AACTCAGCGG CCCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCCCTACA GTCTACTCCC TCACAGCGT GGTGACCGTG  
 CCACAGCACC TTGAGTCCGC GGGACTGGTC GCGGCACGTG TGAAGGGCC GACAGGATGT CAGGAGTCTT GAGATGAGGG AGTCGTCCGA CCACTGGCAC  
 159 V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V  
 1501 CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ATCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGTTCG ACAAGAAAGT TGAGCCCCAA TCTTGTGACA  
 GGGAGGTGGT CGAAGCCGTG GGTCTGGATG TAGACGTTCG ACTTAGTGTT CGGGTCGTTG TGGTTCAGC TGTTCCTTCA ACTCGGGTTT AGAACACTGT  
 192 P S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K  
 1601 AAACCTCAGG CCGCATGAAA CAGCTAGAGG ACAAGGTGCA AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGTG GCAAGACTCA AAAAACTTGT  
 TTTGAGTGCC GCGGTACTTT GTCGATCTCC TGTTCAGCT TCTCGATGAG AGGTTCTTGA TGGTGGATCT CTTACTTCAC CGTTCTGAGT TTTTGAACA  
 226 T H G R M K Q L E D K V E E L L S K N Y H L E N E V A R L K K L V  
 ^end of heavy chain, start of leucine zipper  
 1701 CGGGGAGCGG GGAAGCTTA GTGGCGGTGG CTCTGGTTCC GGTGATTTTG ATTATGAAA GATGGCAAC GCTAATAAGG GGGCTATGAC CGAAATGCCC  
 GCCCTCGGG CCTTTCGAAT CACCGCCACC GAGACCAAGG CCACATAAAC TAATACTTTT CTACCGTTTG CGATTATTC CCGGATCTG GCTTTACGG  
 259 G E R G K L S G G S G D F D Y E K M A N A N K G A M T E N A  
 ^end of leucine zipper  
 ^gene III coat protein (267-end)  
 1801 GATGAAACG CGCTACACTC TGACGCTAAA GGCAACTTG ATTCTGTCG TACTGATTAC GGTGCTGCTA TCGATGGTTT CATTCGTGAC GTTTCGGGCC  
 CTACTTTTGC GCGATGTCAG ACTGGGATTT CCGTTTGAAC TAAGACAGCG ATGACTAATG CCACGACGAT AGCTACCAA GTAACCACTG CAAAGGCCGG  
 292 D E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L  
 1901 TTGCTAATGG TAATGGTGCT ACTGGTGATT TTGCTGGCTC TAATCCCAA ATGGCTCAAG TCGGTGACGG TGATAAATCA CCTTTAATGA ATAAATTCGG  
 AACGATTACC ATTACCAGCA TGACCCTAA AACGACCGAG ATTAAGGGTT TACCGAGTTC AGCCACTGCC ACTATTAACT GGAATTAAGT TATTAAGGC  
 326 A N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R  
 2001 TCAATATTTA CCTTCCCTCC CTCATTCGGT TGAATGTCG CCTTTTGTCT TTAGCGCTGG TAAACCATAT GAATTTTCTA TTGATTTGTA CAAATAAAC  
 AGTTATAAAT GGAAGGGAGG GAGTTAGCCA ACTTACAGCG GGAACACAGA AATCGCGACC ATTTGGTATA CTTAAAGAT AACTAACACT GTTTTATTG  
 359 Q Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N  
 2101 TTATCCCGTG GTGTCCTTTG GTTCTTTTTA TATGTTGCCA CCTTTATGTA TGTATTTCT ACGTTTGCTA ACATACTGG TAATAAGGAG TCTTAA  
 AATAAGGCAC CACAGAAACG CAAAGAAAT ATACAACGGT GGAATACAT ACATAAAGA TGCAACGAT TGTATGACG ATTATCTCTC AGAATT  
 392 L F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

**FIG.\_31C**

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1 GAATTCAACT TCCCATACACT TTGGATAAGG AAATACAGAC ATGAAAATC TCATTGCTGA GTTCTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
  CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGCTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTTCGACGGG TTTTCTTCTT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACACGG GTTGATTGAT CAGGTAGAGG
  CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CCGCTTTTAC TGGTGTGCGC CAACTAACTA GTCCATCTCC

201 GGGCGGTGTA CGAGGTAAAG CCGATGCCA GCATTCCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
  CCGCGGACAT GCTCCATTTC GGCTACGGT CGTAAGGACT GCTGCTATGC CTGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTATTT TTTTAATGTA TTGTAACTA GTACGCAAGT
  TTTTCAATTA GAAAGTTGT CGACAGTATT TCAACAGTGC CCGCTCTGAA TATCAGCGAA ACAAAATAA AAATATACAT AAACATTGAT CATGCGTTCA

401 TCACGTAATA AGGTTATGTA GAGTTGAGG TGATTTTATG AAAAGAATA TCGCATTTCT TCTTCGATCT ATGTTCTGTTT TTTCTATTGC TACAAATGCC
  AGTGCATTTT TCCCATACAT CTCCAACTCC ACTAAATAC TTTTCTTAT AGCGTAAGA AGAAGTGA TACAAGCAAA AAAGATAACG ATGTTTACGG
  0 M K K N I A F L L A S M F V F S I A T N A
    ^start of still signal sequence

501 TATGCAGATA TCCAGATGAC CCAGTCCCCG AGCTCCCTGT CCGCTCTGT GGGCGATAGG GTCACCATCA CCTGCGTGC CAGTCAGGAT GTGTCCACTG
  ATACGCTTAT AGGTTACTG GGTGAGGGC TCGAGGGACA GCGGGAGACA CCCGCTATCC CAGTGGTAGT GGACGGCAGC GTCAGTCCTA CACAGGTGAC
  21 Y A D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q D V S T A
    ^start of light chain
    ^CDR-L1
    ^EcoRV

601 CTGTAGCTG GTATCAACAG AAACCAGGAA AAGCTCCGAA GCTTCTGATT TACTCGGCAT CCTTCCTCTA CTCTGGAGTC CTTCTCGCT TCTCTGGTAG
  GACATCGGAC CATAGTTGTC TTTGGTCCCTT TTCGAGGCTT CGAAGACTAA ATGAGCCGTA GGAAGGAGAT GAGACCTCAG GGAAGAGCGA AGAGACCATC
  55 V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G S
    ^CDR-L2

701 CGGTTCCGGG ACGGATTTCA CTCTGACCAT CAGCAGTCTG CAGCCGGAAG ACTTCGCAAC TTATTACTGT CAGCAATCTT ATACTACTCC TCCCACGTTT
  GCCAAGGCCC TGCCFAAAGT GAGACTGGTA GTGCTCAGAC GTCGGCCTTC TGAAGCGTTG AATAATGACA GTCGTTAGAA TATGATGAGG AGGTTGCAAG
  88 G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F
    ^CDR-L3

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FIG.\_32A

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801 GGACAGGGTA CCAAGGTGGA GATCAAAACGA ACTGTGGCTG CACCATCTGT CTTCATCTTC CCGCATCTG ATGAGCAGTT GAAATCTGGA ACTGCCTCTG  
 CCTGTCCCAT GGTTCACCT CTAGTTTGCT TGACACCCGAC GTGGTAGACA GAAGTAGAAG GCGGGTAGAC TACTCGTCAA CTTTAGACCT TGACGGAGAC  
 121 G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V  
 ^KpnI  
 901 TTGTGTGCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA AGTACACTGG AAGTGGATA ACSCCCTCCA ATCGGGTAAC TCCCAGGAGA GTGTCACAGA  
 AACACACGGA CGACTTATTG AAGATAGGGT CTCTCCGGTT TCATGTCACC TTCCACCTAT TCGGGGAGGT TAGCCCATTG AGGTCCTCTT CACAGTGTCT  
 155 V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E  
 1001 GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA AGTCACCCAT  
 CGTCTGTGCG TTCCTGTGCT GGATGTCGGA GTCGTGCTGG GACTGCGACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TCGGGACGCT TCAGTGGGTA  
 188 Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H  
 1101 CAGGGCCTGA GCTGCCCCGT CACAAAGAGC TTCAACAGGG GAGAGTGTGG TGCCAGCTCC GGTATGGCTG ATCCGAACCG TTTCGCGGCT AAGGACCTGG  
 GTCCCGGACT CGAGCGGGCA GTGTTTCTCG AAGTTGTCTG CTCTCACACC ACGGTGAGG CCATACCGAC TAGGCTTGGC AAAGGCGCCA TTCCTGGACC  
 221 Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L A  
 ^end of light chain, start of gD tag  
 1201 CATAACTCGA GGTGATCCT CTACGCCGGA CGCATCGTGG CCTAGTACG CAAGTTCACG TAAAGAGGT AACTAGAGGT TGAGGTGATT TTATGAAAAA  
 GTATTGAGCT CCGACTAGGA GATGCGGCCT GCGTAGCACC GGGATCATGC GTTCAAGTGC ATTTTCCCA TTGATCTCCA ACTCCACTAA AATACTTTT  
 255 O  
 M K K  
 ^start of stII  
 1301 GAATATCGCA TTTCTTCTTG CATCTATGTT CGTTTTTCT ATTGCTACAA ACGGTACGC TGAGTTTCTG CTGGTGGAGT CTGGCGGTGG CCTGGTGCAG  
 CTTATAGCGT AAAGAAGAAC GTAGATACAA GCAAAAAAGA TAACGATGTT TGCGGATGCG ACTCCAAGTC GACCACCTCA GACCGCCACC GGACACGTC  
 -20 N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G G L V Q  
 ^start of heavy chain  
 ^BsiWI

FIG.\_32B



1401 CCAGGGGGCT CACTCCGTTT GTCTGTGCA GCTTCTGGCT TCACCATAG TGGTCTTGG ATACACTGG TCGTCAAGC CCGGGTAAG GGCCTGGAAT  
 GGTCCCCCGA GTGAGGCAG CAGGACACGT CGAAGACCGA AGTGGTAATC ACCAAGAACC TATGTACCC ACGCAGTCCG GGGCCCATTC CCGGACCTTA  
 14 P G G S L R L S C A A S G F T I S G S W I H W V R Q A P G K G L E W  
 ^CDR-H1  
 1501 GGGTGTGCTG GATTGCTCCT TATAGCGCG CTACTGACTA TGCCGATAGC GTCAAGGGCC GTTTCACAT AAGCGCAGAC ACATCCAAA ACACAGCCTA  
 CCCAACGAAC CTAACGAGGA ATATCGCGC GATGACTGAT ACGCTATCG CAGTTCGCG CAAAGTGATA TTCCGGTCTG TGTAGGTTTT TGTGTCCGAT  
 48 V A W I A P Y S G A T D Y A D S V K G R F T I S A D T S K N T A Y  
 ^CDR-H2  
 1601 CCTACAAATG AACAGCTTAA GAGCTGAGGA CACTGCCGTC TATATATGT CAAGAGAGGG GGGCTTGAT TGGTGTTCG ACTACTGGG TCAAGGAACA  
 GGATGTTTAC TTGTGGAATT CTCGACTCCT GTGACGGCAG ATAATAACAC GTTCTCTCCC CCCGAACATG ACCCACAAGC TGATGACCCC AGTTCTCTGT  
 81 L Q M N S L R A E D T A V Y Y C A R E G G L Y W V F D Y W G Q G T  
 ^CDR-H3  
 1701 CTAGTCACCG TCTCCTCCG CTCCACCAAG GGGCCATCGG TCTTCCCCCT GGCACCTCC TCCAAGAGCA CCTCTGGGG CACAGCGGCC CTGGGCTGCC  
 GATCAGTGGC AGAGGAGCG GAGGTGGTTC CCGGTAGCC AGAGGGGGA CCGTGGGAGG AGGTTCTCGT GGAGACCCCC GTGTCCGCGG GACCCGACGG  
 114 L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C L  
 ^ApaI  
 1801 TGGTCAAGGA CTACTTCCC GAACCGGTGA CGGTGTGCTG GAATCAGGC GGCCTGACCA GCGGCGTGCA CACCTTCCC GCTGTCTTAC AGTCTCAGG  
 ACCAGTTCTT GATGAAGGG CTTGGCCACT GCCACAGCAC CTTGAGTCCG CGGACTGGT CCGCGCACGT GTGGAAGGCG CGACAGGATG TCAGGAGTCC  
 148 V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G  
 1901 ACTCTACTCC CTCAGCAGG TGGTGACCGT GCCCTCCAGC AGCTTGGGA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA CACCAAGGTC  
 TGAGATGAGG GAGTCGTCC ACCACTGCA CCGGAGGTG TCGAACCCGT GGTCTTGGAT GTAGACGTTG CACTTAGTGT TCGGTCGTT GTGGTCCAG  
 181 L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K V  
 2001 GACAAGAAAG TTGAGCCCAA ATCTTGTGAC AAAATCACC TCTAGAGTGG CGGTGGCTCT GGTTCGGTG ATGCTCGTT GCCGCCGGC GTTTTTATG  
 CTGTTCTTTC AACTCGGTT TAGAACACTG TTTTGTAGTGG AGATCTCACC GCCACCGAGA CCAAGGCCAC TACGAGCCAA CCGCGGCCCG CAAAAAATAC  
 214 D K K V E P K S C D K T H L O  
 2101 CTAGCGCGC CCTATACCTT GTCTGCCCTC CCGGCTGCG TCGCGGTGCA TGGAGCCGG CCACCTCGAC CTGAATGGA GCCGGCGCA CCTCGCTAAC  
 GATCGCGCG GGATATGGA CAGACGGAG GCGGCAACG AGCGCACGT ACCTCGGCC GGTGGAGCTG GACTTACCT CCGCGGCCGT GGAGCGATTG

**FIG.\_32C**

2201 GGATTACCA CTCAAGAAT TGGAGCCAAT CAATTCCTTGC GGAGAACTGT GAATGCGCAA ACCAACCCTT GGCAGAACAT ATCCATCGCG TCCGCCATCT  
CCTAAGTGGT GAGGTCTTAA ACCTCGGTTA GTTAAGAAG CCTCTTGACA CTTACGCGTT TGGTTGGGAA CCTCTTGTA TAGGTAGCG AGCGGTTAGA

2301 CCAGCAGCCG CACCGGGCG ATCTCGGGCA GCGTTGGGTC CTGGCCACGG GTGGCGATGA TCGTGCTCCT GTCGTTGAG ACCCGGCTAG GCTGGCGGGG  
GGTCGTCGGC GTGCGCCCGG TAGAGCCCGT CGCAACCCAG GACCGGTGCC CACGCTACT AGCAGGAGA CAGCAACTCC TGGGCCGATC CGACCGCCCC

2401 TTGCCCTTACT GGTAGCAGA ATGAATCACC GATACGCGAG CGAACGTGAA GCGACTGCTG CTGCAAAAACG TCTGCGACCT GAGCAACAAC ATGAATGGTC  
AACGGAATGA CCAATCGTCT TACTTAGTGG CTATGCGCTC GCTTGCACTT CGCTGAGGAC GACGTTTGC AGACGCTGGA CTCGTTGTTG TACTTACCAG

2501 TTCCGCTTCC GTGTTTCGTA AAGTCTGGAA ACGCGGAAGT CAGCGCCCTG CACCATATG TTCCGGATCT GCATCGCAGG ATGCTGCTGG CTACCCCTGTG  
AAGCCAAAGG CACAAAGCAT TTCAGACCTT TCGGCCCTTCA GTCGCGGGAC GTGGTAATAC AAGCCTAGA CGTAGCGTCC TAGCAGACC GATGGGACAC

2601 GAACACCTAC ATCTGTATTA ACGAAGCGCT GGCATTGACC CTGAGTGATT TTCTCTGGT CCGCGCGCAT CCATACCGCC AGTTGTTTAC CCTCACAACG  
CTTGTTGATG TAGACATAAT TGCTTCGGA CCGTAACTGG GACTCACTAA AAGAGACCA GGGCGGCGTA GGTATGGCGG TCAACAAATG GGAGTGTTCG

2701 TTCCAGTAAC CGGCGATGTT CATCATCAGT AACCGTATC GTGAGCATCC TCTCTCGTTT CATCGTATC ATTACCCCCA TGAACAGAAA TTCCCCCTTA  
AAGTCATTG GCCCGTACAA GTAGTAGTCA TTGGGCATAG CACTCGTAGG AGAGAGCAA GTAGCCATAG TAATGGGGGT ACTGTCTTT AAGGGGAAT

2801 CACGAGGCA TCAAGTGACC AACAGGAAA AAACCGCCCT TAACATGGCC CGCTTTATCA GAAGCCAGAC ATTAACGCTT CTGGAGAAAC TCAACGAGCT  
GTGCTCCCGT AGTTCACTGG TTTGTCTTTT TTTGGCGGGA ATTGTACCGG GCGAAATAGT CTTCCGTCTG TAATGCGGA GACCTCTTTG AGTTGCTCGA

2901 GGACGCGGAT GAACAGGCAG ACATCTGTGA ATCGCTTCAC GACCACGCTG ATGAGCTTTA CCGCAGGATC CGGAAATGT AAACGTTAAT ATTTGTGTTAA  
CCTGCCGCTA CTTGTCCGTC TGTAGACACT TAGCGAAGTG CTGGTGGAC TACTCGAAT GCGCTCTAG GCTTTAACA TTTGCAATTA TAAAACAAT

3001 AATTCGCGTT AAATTTTGT TAAATCAGCT CATTTTTTAA CCAATAGGCC GAAATCGCA AAATCCCTTA TAAATCAAAA GAATAGACCG AGATAGGGTT  
TTAAGCGCAA TTTAAAAACA ATTTAGTCGA GTAAAAAT GGTATCCGG CTTTAGCGGT TTTAGGGAAT ATTTAGTTTT CTATCTGGC TCTATCCCAA

3101 GAGTGTGTT CCAGTTTGA ACAAGAGTCC ACTATTAAAG AACGTGGACT CCAACGTCAA AGGCGAAAA ACCGCTATC AGGCTATGG CCCACTACGT  
CTCACACAA GGTCAACCT TGTCTCAGG TGATAATTTC TTGCACCTGA GGTGCACTT TCCCGCTTT TGGCAGATAG TCCGATACC GGTGATGCA

**FIG.\_32D**

3201 GAACCATCAC CCTAATCAAG TTTTTCGGG TCAGGTGCC GTAAAGCACT AAATCGGAAC CCTAAAGGA GCCCCCGATT TAGAGTTGA CGGGAAAGC  
CTTGGTAGTG GGATTAGTTC AAAAAACCC AGCTCCACGG CATTCGTGA TTAGCCCTTG GGATTCCCT CGGGGGCTAA ATCTCGAACT GCCCCTTTCG

3301 CGGCGAACGT GGCAGAGAAAG GAAGGGAAGA AAGCGAAGG AGGGCGCTG CAAGTGTAGC GGTACGCTG CGCGTAACCA CCACACCCGC  
GCCGCTTGCA CCGCTCTTTC CTTCCTCTCT TTCCCTTTCC TCGCCGCGA TCOCGCGACC GTTCACATCG CCAGTGCAC GCGCATTGGT GGTGTGGGCG

3401 CGCGCTTAAT GCGCCGCTAC AGGGCGCTC CGGATCTGC CTCCGCGCTT TCGGTGATGA CCGTGAAAC CTCTGACACA TGCAGTCCC GGAGACGGTC  
GCCGGAATTA CGCGCGATG TCCCGCGGAG GCCTAGGACG GAGCGGCAA AGCCACTACT GCCACTTTG GAGACTGTGT ACGTCGAGG CCTCTGCCAG

3501 ACAGCTTGTG TGTAAGCGA TGCCGGGAGC AGACAGCCCC GTCAGGCGGT GTTGGCGGGT GTCGGGGCGC AGCCATGACC CAGTCACGTA  
TGTCGAACAG ACATTCGCCCT ACGGCCCTCG TCTGTTCCGG CAGTCCGCCA CAACGCCCA CAGCCCCGG TCGGTACTGG GTCAGTGCA

3601 GCGATAGCG AGTGATATACT GGCTTAAC TA GCGGATCA GAGCAGATTG TACTGAGAGT GCACCATATG CCGTGTGAAA TACCGCACAG ATGCGTAAGG  
CGGTATCGCC TCACATAGA CCGAATTGAT ACGCCGTAGT CTCGTCTAAC ATGACTCTCA CGTGGTATAC GCCACACTTT ATGGCGGTG TACGCATTCC

3701 AGAAAATACC GCATCAGGC CTCTTCCGT TCCTCGTCA CTGACTCGT GCGCTCGTC GTTCGGCTG GCGAGCGGT ATCAGTCAAC TCAAAGCGG  
TCTTTTATGG CGTAGTCCG GAGAAGCGA AGGAGCGAGT GACTGAGCGA CCGGAGCCAG CAAGCCGACG CCGCTCGCA TAGTCAGTG AGTTTCCGCC

3801 TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTA GCAAAAGCC AGGAACCGT AAAAAGGCC CGTTGCTGGC  
ATTATGCCAA TAGGTGTCTT AGTCCCTAT AGTCCCTAT TGCGTCTCTT CTGTGACT CTGTTTCCG TCGTTTCCG GTCCTTGGCA TTTTTCGGC GCAACGACCG

3901 GTTTTTCAT AGGCTCCGC CCCCTGACGA GCATCAAAA AATCAGCGT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC TATAAAGATA CCAGCGGTTT  
CAAAAAGTA TCCGAGGCG GGGACTGCT CGTAGTGT TTAGTGCGA GTTCAGTCTC CACCGCTTG GGCTGTCTG ATATTCTAT GGTCCGAAA

4001 CCCCCGGAA GCTCCCTCGT GCGCTCTCT GTTCCGACCC TGCCGCTTAC CGGATACCTG TCCCTTCGGG AAGCGTGGC CTTTCTCATA  
GGGGACCTT CGAGGGAGCA CGCGAGAGA CAAGGCTGGG ACGCGAATG GCCTATGGAC AGGCGAAG AGGGAAGCCC TTCGCACCGC GAAAGATAT

4101 GGTACAGCTG TAGGTATCT AGTTCGGTGT AGTCCAGCTG GGTGTGTG CCGAACCCC CGTTCAGCCC GACCGTGGC CTTATCCGG  
CGAGTCCGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC GAGGTTCGAC CCGACACAG TGCTTGGGG GCAAGTCCGG CTGGCGACGC GGAATAGGCC

4201 TAACTATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT  
ATTGATAGCA GAACTCAGGT TGGGCCATT TGTGCTGAAT AGCGGTGACC GTGCTCGGT ACCATTGTCC TAATCGTCTC GTCCTATACA TCCGCCACGA

**FIG.\_32E**

4301 ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA GAAGGACAGT AATTGGTATC TGGGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG  
 TGTCTCAAGA ACTTCACCAC CGGATTGATG CCGATGTGAT CTTCCTGTCA TAAACCATAG ACGGAGACG ACTTCGGTCA ATGGAAGCCT TTTTCTCAAC  
  
 4401 GTAGCTCTTG ATCCGGCAAA CAAACCACG CTGGTAGCGG TGGTTTTTTT GTTGAAGC ACCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC  
 CATCGAGAAC TAGGCCGTTT GTTTGGTGGC GACCATCGCC ACCAAAAAAA CAAACGTTCC TCGTCTAATG CCGGTCITTTT TTTCCCTAGAG TTCTTCTAGG  
  
 4501 TTTGATCTTT TCTACGGGGT CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGATTTT GGTCAATGAG TTATCAAAAA GGATCTTCAC CTAGATCCTT  
 AAACAGAAA AGATGCCCCA GACTGCGAGT CACCTTGCTT TTGAGTGCAA TTCCCTAAAA CCAGTACTCT AATAGTTTTT CCTAGAGTG GATCTAGGAA  
  
 4601 TTAAATTTAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGACTAATC TTGGTCTGAC AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA  
 AATTAAATTT TTACTTTCAA ATTTAGTTAG ATTTTCATATA TACTCATTTG AACAGACTG TCAATGGTTA CGAATTAGTC ACTCCGTGGA TAGAGTCGCT  
  
 4701 TCTGTCTATT TCGTTCATCC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT ACCATCTGSC CCCAGTCTG CAATGATACC  
 AGACAGATAA AGCAAGTAGG TATCAACGGA CTGAGGGGCA GCACATCTAT TGATGCTATG CCTCCCGAA TGGTAGACCG GGGTCACGAC GTTACTATGG  
  
 4801 GCGAGACCCA CGCTCACCGG CTCCAGATTT ATCAGCAATA AACAGGCCAG CCGGAAGGC CGAGCGCAGA AGTGGTCCCTG CAACTTTATC CGCCTCCATC  
 CGCTCTGGGT GCGAGTGGCC GAGGTCTAAA TAGTCGTTAT TTGGTCGGTC GGCTTCCCG GCTCGGCTCT TCACCAGGAC GTTGAATAG GCGGAGGTAG  
  
 4901 CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGGC AACGTTGTTG CCATTGCTGC AGGCATCGTG GTGTACGCT  
 GTCAGATAAT TAACAACGGC CCTTCGATCT CATTCATCAA GCGGTCAATT ATCAAAACGG TTGCAACAAC GGTAACGAGG TCCGTAGCAC CACAGTCCGA  
  
 5001 CGTCGTTTGG TATGGCTTCA TTCAGTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC  
 GCAGCAAAAC ATACCGAAGT AAGTCGAGC CAAGGGTTGC TAGTTCCGCT CATGTACTA GGGGGTACAA CACGTTTTTT CGCCAATCGA GGAAGCCAGG  
  
 5101 TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTATATCA CTCATGGTTA TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT AAGATGCTTT  
 AGGCTAGCAA CAGTCTTCAT TCAACCGGCG TCACAAATAGT GAGTACCAAT ACCGTCTGTA CGTATTAGA GAATCACAGT ACGGTAGGCA TTCTACGAAA  
  
 5201 TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG GCGACCGAGT TGCTCTTGCC CGGCGTCAAC ACGGGATAAT ACCGCGCCAC  
 AGACACTGAC CACTCATGAG TTGGTTCACT AAGACTTTA TCACATACGC CGTGGCTCA ACGAGAACGG GCCGCGATTG TGCCCTATTA TGGCGCGGTG

**FIG.\_32F**

5301 ATAGCAGAAC TTTAAAGTG CTCATCATTTG GAAACGTTT TCCGGGGCGA AAACCTCTCAA GGATCTTACC GCTGTTGAGA TCCAGTTTCCA TGTAACCCAC  
 TATCGTCTTG AAATTTTCAC GAGTAGTAAC CTTTGTGCAAG AAGCCCCGGCT TTTGAGAGTTT CCTAGAAATGG CGACAACTCT AGGTCAAGCT ACATTGGGTG  
 5401 TCGTGCACCC AACTGATCTT CAGCATCTTT TACTTTTACC AGCGTTTCTG GGTGAGCAGA AACAGGAAGG CAAAAAGGG AATAAGGGGG  
 AGCAGCTGGG TTGACTAGAA GTGCTAGAAA ATGAAAGTGG TCGCAAGAC CCACTCGTTT TTGTCCTTCC GTTTTACGGC GTTTTCTCC TTATTCCCGC  
 5501 ACACGGAAAT GTTGAATACT CATACTCTT CTTTTCATAT ATTATTGAAG CATTATACAG GGTATTGTG TCATGAGCGG ATACATATTT GAATGTATTT  
 TGTGCCCTTA CAACCTATGA GTATGAGAAG GAAAAAGTTA TAATAACTTC GTAAATAGTC CCAATAACAG AGTACTCGCC TATGTATATA CTTACATATA  
 5601 AGAAAAATAA ACAAAATAGG GTTCCGGCGA CATTTCCTCCG AAAAGTGCCA CCTGACGCTT AAGAAACCAT TATTATCATG ACATTAACCT ATAAAAATAG  
 TCTTTTATTT TGTTTATCCC CAAGGCGCGT GTAAAGGGG TTTTACCGGT GGAATGCGA TTCCTTTGTA ATAATAGTAC TGTAAATGGA TATTTTATC  
 5701 GCGTATCAG AGGCCCTTTC GTCTTCAATA CAGGTAGACC TTTCCGTAGAG ATGTACAGTG AAATCCCCGA AATTATACAC ATGACTGAAG GAAGGGAGCT  
 CGCATAGTGC TCCGGGAAAG CAGAAGTTAT GTCCATCTGG AAAGCATCTC TACATGTAC TTTAGGGGCT TTAATATGTG TACTGACTTC CTTCCCTCGA  
 5801 CGTCATTCCC TGCCGGGTTA CGTCACCTAA CATCACTGTT ACTTTAAAA AGTTTCCACT TGACACTTTG ATCCCTGATG GAAAACGCAT AATCTGGGAC  
 GCAGTAAGG ACGGCCCAAT GCAGTGGATT GTAGTGACAA TGAATTTT TCAAAGGTGA ACTGTGAAAC TAGGGACTAC CTTTTCGCTA TTAGACCCCTG  
 5901 AGTAGAAGG GCTTCATCAT ATCAAAATGCA ACGTACAAAG AAATAGGGCT TCTGACCTGT GAAGCAACAG TCAATGGGCA TTTGTATAAG ACAAACTATC  
 TCATCTTCC CGAAGTAGTA TAGTTTACGT TGCAATGTTT TTTATCCCGA AGACTGGACA CTTCTGTTGT AGTTACCCGT AAACATATTC TGTGTGATAG  
 6001 TCACACATCG ACAAAACCAAT ACAATACAGG TAGACCTTTC GTAGAGATGT ACAGTGAAT CCCCAGAAAT ATACACATGA CTGAAGGAAG GGAGCTCGTC  
 AGTGTGTAGC TGTTTGGTTA TGTATGTCTC ATCTGGAAG CATCTCTACA TGTCACTTTA GGGGCTTTAA TATGTGTACT GACTTCTTTC CCTCGAGCAG  
 6101 ATTCCCTGCC GGGTTACGTC ACCTAACATC ACTGTTACTT TAAAAAGTT TCCACITTCAC ACTTTGATCC CTGATGGAAA ACGCATATC TGGGACAGTA  
 TAAGGGACGG CCCAATGCAG TGGATTGTAG TGACAATGAA ATTTTTCCTTCAA AGGTGAACCTG TGAACCTTAGG GACTACCTTT TGCCTATTAG ACCCTGTCTCAT  
 6201 GAAAGGGCTT CATCATATCA AATGCAACGT ACAAGAAAT AGGGCTTCTG ACCTGTGAAG CAACAGTCAA TGGGCATTTG TATAAGACAA ACTATCTCAC  
 CTTTCCCGAA GTAGTATAGT TTACGTTGCA TGTCTCTTTA TCCCGAAGAC TGGACACTTC GTTGTCTAGTT ACCCGTAAAC ATATTCTGTT TGATAGAGTG  
 6301 ACATCGACAA ACCAATACAA TCTACAGGTA GACCTTTCTG AGAGATGTAC AGTGAATCC CCGAAATTTAT ACACATGACT GAAGGAAGGG AGCTCGTCTCAT  
 TGTAGCTGTT TGGTTATGTT AGATGTCCAT CTGGAAGCA TCTCTACATG TCACCTTTAGG GGGTTTAAATA TGTGTACTGA CTTCTCTTCC TCGAGCAGTA  
 6401 TCCCTGCCGG GTTACGTCAC CTAACATCAC TGTACTTTA AAAAGTTTC CACTTGACAC TTTGATCCCT GATGAAAAC GCATAATCTG GGACAGTAGA  
 AGGACGGCC CAATGCAGTG GATTGTAGTG ACAATGAAT TTTTTCAAAG GTGAACCTGTG AAACCTAGGA CTACCTTTTG CGTATTAGAC CCTGTCTATCT  
 6501 AAGGGCTTCA TCATATCAAA TGCACAGTAC AAGAAATAG GGCTTCTGAC CTGTGAAGCA ACAGTCAATG GGCATTTGTA TAAGACAAAC TATCTCACAC  
 TTCCCGAAGT AGTATAGTTT ACGTTGCATG TTTCTTTATC CCGAAGACTG GACACTTCTG TGTCAAGTAC CCGTAAACAT ATTCTGTTTG ATAGAGTGTG  
 6601 ATCGACAAAC CAATACAATC  
 TAGCTGTTTG GTTATGTTAG

**FIG. 32G**

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1  TTCGAGCTCG CCGGACATTG ATTATTGACT AGTTATTAAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCATATAT GGAGTTCGC GTTACATAAC
   AAGCTCGAGC GGGCTGTAACT TAATAACTGA TCAATAATTA TCATTAGTGA ATGCCCCAGT AATCAAGTAT CGGGTATATA CCTCAAGGCG CAATGTAATTG

101 TTACGGTAAA TGGCCCGCCT GGCCTGACCG CCAACGACCC CCGCCCATTTG ACCTCAATAA TGACCTATGT TCCCATAGTA ACGCCAATAG GGAATTTCCTA
   AATGCCATTT ACCGGCGGGA CCGACTGGCG GGTGCTGGG GCGGGGTAACT TGCAGTTATT ACTGCATACA AGGGTATCAT TCGGGTTATC CCTGAAAGGT

201 TTGACGTCAA TGGGTGGAGT ATTTACGGTA AACTGCCAC AACTGCCAGTAC TTGGCAGTAC TCATATGCCA AGTACGCCC CTATTGACGT CAATGACGGT
   AACTGCAGTT ACCACCTCA TAAATGCCAT TTGACGGGTG AACCGTCAAT TAGTTCACAT AGTATACGGT TCATGCGGG GATAACTGCA GTTACTGCCA

301 AAATGGCCCG CCTGGCATTA TGCCCAGTAC ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC
   TTTACCGGGC GGACCGTAAT ACGGTCATG TACTGGAATA CCTGAAAGG ATGAACCGTC ATGTAGATGC ATATCAGTA GCGATAATGG TACCACCTAGC

401 GGTTTTGGCA GTACATCAAT GGGCGTGGAT ACGCGTTTGA CTCACGGGGA TTTCCAACTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA
   CAAAACCGT CATGTAGTTA CCGCACCTA TCGCCAACT GAGTGCCCT AAAGTTTAC AGGTGGGGTA ACTGCAGTTA CCTCAAACA AAACCGTGGT

501 AAATCAACGG GACTTTTCCAA AATGTCGTAA CAATCCGCC CCATTGACG AATGGGGG TAGGCGTGT TCTATATAAG CAGAGTCTCGT
   TTTAGTTGCC CTGAAAGGTT TTACAGCATT GTTGGGGCG GGTAACTGCG TTTACCGGCC ATCCGCACAT GCCACCTCC AGATATATTC GTCTCGAGCA

601 TTAGTGAACC GTCAGATCGC CTGGAGACGC CATCCACGCT GTTTTGACCT CCATAGAAGA CACCGGGACC GATCCAGCCT CCGCGGCGG GAACGGTGCA
   AATCACCTGG CAGTCTAGCG GACCTCTGCG GTAGGTGCGA CAAACTGGA GGTATCTTCT GTGGCCCTGG CTAGTTCGGA GCGCGCGGCC CTTGCCACGT

701 TTGGAACGGG GATTCGCCGT GCCAAGAGTG ACCTAAGTAC CGCCTATAGA GTCTATAGG CCACCCCTTT GGCTTCGTTA GAACGGGGCT ACAATTAATA
   AACCTTGCGC CTAAGGGGCA CGGTCTCTAC TGCAATTCATG GCGGATATCT CAGATATCCG GGTGGGGGAA CCGAAGCAAT CTGCGCGCGA TGTTAATTAT

801 CATAACCTTA TGTATCATAC ACATACGATT TAGGTGACAC TATAGAATAA CATCCACTTT GCCTTTCTCT CCACAGGTGT CCACCTCCAG GTCCAACCTGC
   GTATTGGAT ACATAGTATG TGTATGCTAA ATCCACTGTG ATATCTTATT GTAGGTGAAA CCGAAGAGA GGTCTCCACA GTGAGGGTC CAGGTTGACG

901 ACCTCGGTC TATCGATTGA ATTCACCAT GGGATGGTCA TGTATCATCC TTTTCTTAGT AGCAACTGCA ACTGAGTAC ATTACAGATAT CCAGATGACC
   TGGAGCCAAG ATAGCTAACT TAAGTGGTA CCTACCAGT ACATAGTAGG AAAAAGATCA TCGTTGACGT TGACCTCATG TAAGTCTATA GGTCTACTGG

1  M G W S C I I L F L V A T A T G V H S D I Q M T
   ^met ^Start VL ^EcorV

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FIG.\_33A

55 / 74

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1001 CAGTCCCCGA GCTCCCTGTG CGCTCTGTG GCGGATAGG TCACCATCAC CTGCCGTGCC AGTCAGGATG TGTCACACTGC TGTCAGCCTGG TATCAACAGA
    GTACAGGGCT CGAGGACAG GCGGAGACAC CCGCTATCCC AGTGGTAGTG GACGGCAGG TCAGTCTCTAC ACAGTGACG ACATCGGACC ATAGTTGTCT
25 Q S P S S L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K
    ^CDR-L1

1101 AACACGAAA AGCTCCGAAG CTTCTGATTT ACTCGGCATC CTTCTCTCTAC TCTGGACTCC CTTCTCGCTT CTCTGGTAGC GGTTCGGGA CGGATTTTCC
    TTGGTCTCTTT TCGAGGCTTC GAAGACTAAA TGAGCCGTAG GAAGGAGATG AGACCTCAGG GAAGAGCGAA GAGACCATCG CCAAGGCCCT GCCTAAAGTG
59 P G K A P K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T
    ^CDR-L2

1201 TCTGACCATC AGCAGTCTGC AGCCGGAAGA CTTCCGCACT TATTACTGTC AGCAATCTTA TACTACTCCT CCCACGTTTC GACAGGGTAC CAAGGTGGAG
    AGACTGGTAG TCGTCAGACG TCGGCCCTTCT GAAGCGTTGA ATAATGACAG TCGTTAGAAT ATGATGAGGA GGGTGCAAGC CTGTCCCATG GTTCCACCTC
92 L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E
    ^CDR-L3
    ^Kpni

1301 ATCAACGAA CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA TGAGCACTTG AAATCTGGAA CTGCTTCTGT TGTGTGCCTG CTGAATAACT
    TAGTTTGCTT GACACCGACG TGCTAGACAG AAGTAGAAGG GCGGTAGACT ACTCGTCAAC TTTAGACCTT GACGAAGACA ACACACGGAC GACTTATTGA
125 I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F
    ^start human kappa

1401 TCTATCCCAG AGAGGCCAAA GTACAGTGGA AGGTGGATAA CGCCCTCCAA TCGGGTAACT CCCAGGAGAG TGTCACAGAG CAGGACAGCA AGGACAGCAC
    AGATAGGGTC TCTCCGGTTT CATGTCACCT TCCACCTATT CCGGGAGGTT AGCCCATTTGA GGGTCTCTCTC ACAGTGTCTC GTCTGTCTGT TCCTGTCTGTG
159 Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T

1501 CTACAGCCTC AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAAC ACAAGTCTA CGCTTCCGAA GTACCCCATC AGGGCCTGAG CTCGCCCGTC
    GATGTCGGAG TCGTCGTGGG ACTGCGACTC GTTTCGTCTG ATGCTCTTTG TGTTCAGAT GCGGAGGCTT CAGTGGGTAG TCCCGGACTC GAGCGGGCAG
192 Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V

1601 ACAAGAGCT TCAACAGGGG AGAGTGTTAA GCTTGGCCGC CATGGCCCAA CTGTGTTATT GCAGTTATA ATGTTTACAA ATAAAGCAAT AGCATCACAA
    TGTGTTCTGA AGTTGTCCCC TCTCACAATT CGAACCAGCG GTACCGGGTT GAACAATAA CGTCCAATAT TACCAATGTT TATTTCGTTA TCGTAGTGTT
225 T K S F N R G E C O

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**FIG.\_33B**

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1701 ATTTACAAA TAAAGCATTT TTTTCACTGC ATTCTAGTTG TGGTTTGTC AAATCATCA ATGTATCTTA TCATGTCTGG ATCGGGAATT AATTCGGCGC
TAAAGTGTTT ATTTCTGTA AAAAGTGACG TAAGATCAAC ACCAAACAGG TTTGAGTAGT TACATAGAAT AGTACAGACC TAGCCCTTAA TTAAGCCGCG
1801 AGCACCATGG CCTCTGAATA CCTCTGAAAG AGGAACTTGG TTAGGTATCT TCTGAGCGGG AAAGAACCAG CTCGTGGAATG TGTGTCAAGT AGGTTGTGGA
TCGTGGTACC GGACTTTATT GGAGACTTTC TCCTTGAACC AATCCATAGA AGACTCCGCC TTTCTTGGTC GACACCTTAC ACACAGTCAA TCCCACACCT
*change from C to T, kill KpnI site
1901 AAGTCCCCAG GCTCCCCCAG AGCAGAAAGT ATGCAAGCA TGCATCTCAA TTAGTCAGCA ACCAGTGTG GAAAGTCCCC AGGTCCCCA GCAGGCAGAA
TTCAGGGGTC CGAGGGGTG TCCGTCTTCA TACGTTTCGT ACGTAGAGTT AATCAGTCGT TGGTCCACAC CTTTCAGGGG TCCGAGGGGT CGTCCGTCTT
2001 GTATGCAAG CATGCATCTC AATTAGTCAG CAACCATAGT CCGCCCCCTA ACTCCGCCCA TCCCGCCCT AACTCCGCC AGTTCGCCC ATTCTCCGCC
CATACGTTTC GTACGTAGAG TTAATCAGTC GTTGGTATCA GGGCGGGGT TGAGGCGGG TCAAGGCGGG TTAAGAGGCGG
2101 CCATGGCTGA CTAATTTTTT TTAATTTATG AGAGGCGGAG GCGGCTCGG CCTCTGAGCT ATTCCAGAAG TAGTCAGGAG GCTTTTGTGG AGGCCTAGGC
GGTACCGACT GATTAAAAAA AATAAATAG TCTCCGGCTC CGCGGAGCC GGAGACTCGA TAAGGTCTTC ATCACTCTC CGAAAAAAC TCCGGATCCG
2201 TTTTGC AAAA AGCTGTAAAC AGCTTGGCAC TGSCCGTCTG TTTACAACGT CGTACTGGG AAAACCTGG CGTTACCCAA CTTAATCGCC TTGCAGCACA
AAACGTTTT TCGACAATTG TCGAACCGTG ACCGGCAGCA AATGTTGCA GCACGTAGCC TTTTGGGACC GCAATGGGTT GAATTAGCGG AACGTCGTGT
2301 TCCCCCCTTC GCCAGTGGC GTAATAGCGA AGAGGCCCGC ACCGATCGC CTTCGCCACA GTTGCCTAGC CTGAATGGCG AATGGCGCCT GATCGGGTAT
AGGGGGGAAG CGGTCCACCG CATTATCGCT TCTCCGGGCG TGGCTAGCG GAAGGTTCT CAACGCATCG GACTTACCG TTACCGCGGA CTACGCCATA
2401 TTTCTCCTTA CGCATCTGTG CGGTATTTC AACCGCATAC GTCAAAGCAA CCATAGTAG CGCCCTGTAG CGGCGCATTA AGCGCGCGG GTGTGGTGGT
AAAGAGGAAT GCGTAGACAC GCCATAAAGT GTGGCGTATG CAGTTTCGTT GGTATCATGC GCGGGACATC GCCGCGTAAT TCGGCGCCGC CACACCACCA
2501 TACGCGCAGC GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCGCTCCTT TCGCTTCTCT CCTTCTCTTT CTCGCCACGT TCGCGCGCTT TCCCCGTCAA
ATGCGCGTCG CACTGGCGAT GTGAACGGTC GCGGATCGC GGGCGAGGAA AGCGAAGAAA GAGCGGTGCA AGCGCCGAA AGGGCAGTT
2601 GCTCTAATC GGGGGCTCCC TTTAGGGTTC CGATTTAGTG CTTTACGGCA CCTCGACCCC AAAAAGCTTG ATTTGGGTGA TGGTTACGT AGTGGGCCAT
CGAGATTAG CCCCCGAGG AATCCCAAG GCTAAATCAC GAAATGCCGT GGAGCTGGG TTTTGTGAAC TAAACCCACT ACCAAGTGA TCACCCGGTA

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**FIG. 33C**



2701 CGCCCTGATA GACGGTTTTT CGCCCTTTGA CGTTGGAGTC CACGTTCTTT AATAGTGGAC TCCTGTTCCTCA AACGTGAACA AACTCAACC CTATCTCGG  
 GCGGGACTAT CTGCCAAAA GCGGAAACT GCAACCTCAG GTGCAAGAAA TTATCACTG AGAACAGGT TTGACCTTGT TGTAGTTGG GATAGAGCCC  
  
 2801 CTATTTCTTTT GATTTATAAG GGATTTTGGC GATTTCTGCC TATTTGGTTAA AAAATGAGCT GATTTAACAA AAATTTAACG CGAATTTTAA CAAAAATATTA  
 GATAAGAAAA CTAAATATTC CCTAAACCG CTAAAGCCGG ATAACCAATT TTTTACTCGA CTAAATGT TTTHAAATGCG GCTTAAATTT GTTTTATAAT  
  
 2901 ACGTTTACAA TTTTATGGTG CACTCTCAGT ACAATCTGCT CTGATGCCG ATAGTTAAGC CAATCCGCT ATCGTACGT GACTGGGTCA TGGCTGCGCC  
 TGCAATGTT AAAATACCAC GTGAGAGTCA TGTTAGACGA GACTACGGCG TATCAATTCG GTTAGGCGA TAGCATGCA CTGACCCAGT ACGGACGCGG  
  
 3001 CCGACACCCG CCAACACCCG CTGACGCGCC CTGACGGGCT TGTCTGCTCC CGGCATCCG TTACAGACAA GCTGTGACCG TCCTCCGGGAG CTGCATGTGT  
 GGCTGTGGGC GGTGTGGGC GACTGCGGG GACTGCCCGA ACAGACGAGG GCGTAGGCG AATGCTGT TTGACACTGGC AGAGGCCCTC GACGTACACA  
  
 3101 CAGAGTTTTT CACCGTCATC ACCGAAACG CCGAGGCGCT ATTCTTGAAG ACGAAAGGC CTCGTGATAC GCCTATTTTT ATAGGTTAAT GTCATGATAA  
 GTCTCCAAAA GTGGCAGTAG TGGCTTTGG CGCTCCGTCA TAAGAACCTC TGCTTTCCCG GAGCACTATG CGGATAAAAA TATCCAATTA CAGTACTATT  
  
 3201 TAATGGTTTC TTAGACGTCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA ACCCTATTT GTTTATTTTT CTAATACAT TCAAATATGT ATCCGCTCAT  
 ATTACAAAG AATCTGCAGT CCACCGTGAA AAGCCCTTT ACACGCGCCT TGGGGATAAA CAAATAAAAA GATTATGTA AGTTATACA TAGGCGAGTA  
  
 3301 GAGACAATAA CCCTGATAA TGCTTCAATA ATATTGAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT GTCGCCCTTA TTCCCTTTTT TCGGGCATTT  
 CTCCTTTATT GGGACTATTT ACGAAGTTAT TATACTTTTT TCCTTCTCAT ACTCATAGT TGTAAAGCA CAGCGGGAAT AAGGAAAAA ACGCCGTAAA  
  
 3401 TGCCCTCCTG TTTTGTCTCA CCCAGAAACG CTGGTGAAAG TAAAGATGC TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA  
 ACGGAAGGAC AAAAACGAGT GGTCTTTTGC GACCCTTTC ATTTCTTACG ACTTCTAGTC AACCCACGTG CTCACCCAAT GTAGCTTGAC CTAGAGTTGT  
  
 3501 GCGGTAAGAT CCTTGAGAGT TTTGCGCCCG AAGAACGTTT TCCAATGATG AGCATTTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTGATGACGC  
 CGCCATTCTA GGAATCTCA AAAGCGGGG TTCTTGCAA AGGTTACTAC TCGTGAAAT TTCAAGACGA TACACCGCGC CATAATAGG CACTACTGCG  
  
 3601 CCGGCAAGAG CAATCGGTC GCCCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTACA GAAAGCATC TTACGGATGG CATGACAGTA  
 GCGCGTCTC GTTGAGCCAG CCGCGTATGT GATAAGATC TTACTGAACC AACTCATGAG TGGTCAGTGT CTTTTCGTAG AATGCCATCC GTACTGTCTAT

**FIG.\_33D**

3701 AGAGAATTAT GCAGTGCTGC CATAACCATG AGTGATAACA CTGCGGCCAA CTTACTTCTG ACAAGCATCG GAGGACCGAA GGAGCTAACC GCTTTTTTGC  
TCTCTTAATA CGTCACGACG GTATTGGTAC TCACTATTGT GACGCCGGTT GAATGAAGAC TGTGTCTAGC CTCCTGGCTT CCTCGATTGG CGAAAAACG

3801 ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAAAACGA CGAGCGTGAC ACCACGATGC CAGCAGCAAT  
TGTTGTACCC CCTAGTACAT TGAGCGGAAC TAGCAACCC TGGCCTCGAC TTACTTCGGT ATGTTTGCT GTCGCACTG TGGTGCTACG GTCGTGCTTA

3901 GGCACAACG TTCCGCCAAC TATTAACTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA  
CCGTTGTTGC AACCGGTTG ATAAATTGACC GCTTGATGAA TGAGATCGAA GGGCCGTGT TAATTATCTG ACCTACCTCC GCCTATTCA ACGTCTGGT

4001 CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCCGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG GGGCCAGATG  
GAAGACGCGA GCGGGGAGG CCGACCGACC AAATAACGAC TATTTAGACC TCGGCCACTC GCACCCAGAG CGCCATAGTA ACGTCTGTGAC CCCGTTCTAC

4101 GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC GAATAPAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA  
CATTCGGGAG GGCATAGCAT CAATAGATGT GCTGCCCTC AGTCCGTTGA TACCTACTTG CTTTATCTGT CTAGCGACTC TATCCACGGA GTGACTAATT

4201 GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAACTTCA TTTTAAATTT AAAAGGATCT AGGTGAAGAT CCTTTTTGAT  
CGTAACCATT GACAGTCTGG TTCAAATGAG TATATATGAA ATCTAACTAA ATTTGAACT AAAATTAAG TTTTCCTAGA TCCACTTCTA GGAAAACTA

4301 AATCTCATGA CCAAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCCTC AGACCCCGTA GAAAGATCA AAGGATCTC TTGAGATCCT TTTTCTCTGC  
TTAGAGTACT GGTTTTAGGG AATTGCAC TC AAAAGCAAGG TGACTCGCAG TCTGGGGCAT CTTTCTTAGT TTCTAGAG AACTCTAGGA AAAAAGAGC

4401 GCGTAACTG CTGTTTCAA ACAAAAAAC CACCGCTACC AGCGGTGGTT TGTTCGCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT  
CGCATTAGAC GACCAACGTT TGTTTTTTTG GTGGCGATGG TCGCCACCAA ACAACGGCC TAGTTCTCGA TGGTTGAGAA AAAGGCTTCC ATTGACCGAA

4501 CAGCAGAGCG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA  
GTCGTCGCG GTCTATGGTT TATGACAGGA AGATCACATC GGCATCAATC CCGTGGTGAA GTTCTGTAGA CATCGTGGCG GATGTATGGA GCGAGACGAT

4601 ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCTG GTCTTACCGG GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA  
TAGGACAATG GTCACCGACG ACGGTCAACG CTATTACGCA CAGAATGGCC CAACCTGAGT TCTGTATCA ATGSOCTATT CCGGTGCGCC AGCCCGACTT

**FIG.\_33E**

4701 CCGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC TACAGGCTGA GCATTGAGAA AGCGCCACGC TTCCCGAAGG  
GCCCCCAAG CACGTGTGC GGTGGAACC TCGCTTGCTG GATGTGGCTT GACTCTATGG ATGTGCACT CGTAACTCTT TCGCGGTGCG AAGGGCTTCC

4801 GAGAAAGCGG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCCAGGG GGAACGGCTT GGTATCTTTA TAGTCCCTGT  
CTCTTTCCGC CTGTCCATAG GCCATTGCGG GTCCCAGCCT TGTCTCTCTG CGTGTCTCCT CGAAGGTCCC CCTTTGCGGA CCATAGAAAT ATCAGGACAG

4901 GGGTTTCGCC ACCTCTGACT TGAGCGTCTGA TTTTGTGTAT GCTCGTCTAG GGGCGGAGC CTATGGAATA ACGCCAGCAA CGCGGCCCTT TTACGGTTCC  
CCCAAGCGG TGGAGACTGA ACTCGCAGCT AAAACACTA CGAGCAGTCC CCGCGCTCTG GATACCTTTT TCGGGTCGTT GCGCCGGA AATGCCAAGG

5001 TGGCCTTTTG CTGGCCTTTT GCTCACATGT TCTTCTCTGC GTTATCCCTT GATTCTGTGG ATACCGTAT TACCGCCTTT GAGTGAGCTG ATACCGCTCG  
ACCGGAAAC GACCGGAAA CGAGTGTACA AGAAGGAGC CAATAGGGA CTAAGACACC TATTGCGATA ATGCGGAAA CTCACCTCGAC TATGGCGAGC

5101 CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCGGAG AGCGCCCAAT ACGCAACCG CCTCTCCCCG CCGGTTGGCC GATTCATTAA  
GGCGTCGGCT TGCCTGGCTCG CGTCGCTCAG TCACTCGCTC CTTCGCCCTTC TCGCGGGTTA TCGGTTTGGC GGAGAGGGGC GCGCAACCGG CTAAGTAATT

5201 TCCAGCTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGA GTGAGCGGCA CGCAATTAAAT GTGAGTTACC TCACTCATTG GGCACCCCGG GCTTTACACT  
AGGTGACCG TGCTGTCCAA AGGGCTGACC TTTCGCCCGT CACTCGCGTT GCGTTAATTA CACTCAATGG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA

5301 TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATTAA  
AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC TATTGTTAAA GTGTGCTCTT TGTGATACT GTACTAATG CTTAATT

**FIG.\_33F**

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1  ATTCGAGCTC GCGCGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTTCAT AGCCCATATA TGGAGTTCCG CGTTACATAA
   TAAGTCGAG CCGGCTGTAA CTAATAACTG ATCAATAATT ATCATTAGTT AATGCCCCAG TAATCAAGTA TCGGGTATAT ACCTCAAGGC GCAATGTATT

101 CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAACGACC CCGGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC
   GAATGCCATT TACCGGGCGG ACCGACTGGC GGGTTGCTGG GGGCGGGTAA CTGCAGTTAT TACTGCATAC AAGGGTATCA TTCCGGTTAT CCCTGAAAGG

201 ATTACAGTCA ATGGGTGGAG TATTACGGT AAACCTGCCA CTGGCAGTA CATCAAGTGT ATCATATGCC AAGTAGCCCC CCTATTGACG TCAATGACGG
   TAACTGCAGT TACCCACCTC ATAAATGCCA TTTGACGGGT GAACCGTCAT GTAGTTCACA TAGTATACGG TTCATGCGGG GGATAACTGC AGTTACTGCC

301 TAAATGGCCC GCCTGGCATT ATGCCCAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA GTATCTATAC TCGCTATTAC CATGGTGATG
   ATTTACCGGG CCGACCGTAA TACGGGTCAAT GTACTGGAAT ACCCTGGAAG GATGAACCGT CATGTAGATG CATAATCAGT AGCGATAATG GTACCACTAC

401 CGGTTTGGC AGTACATCAA TGGGCGTGGG TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA TGGGAGTTTG TTTTGGCACC
   GCCAAAACCG TCATGTAGTT ACCCGCACCT ATCGCCCAAC TGAGTGCCCC TAAAGTTCA GAGTGGGGT AACTGCAGTT ACCCTCAAAC AAAACCGTGG

501 AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC CCATTGACG CAAATGGGGG GTAGCGGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCG
   TTTTAGTTGC CCGTAAAGGT TTTACAGCAT TGTTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC CAGATATATT CGTCTCGAGC

601 TTTTAGTGAAC CGTCAGATCG CCTGGAGACG CCATCCACGC TGTTTTGACC TCCATAGAAG ACACCGGGAC CGATCCAGCC TCCGCGGCGG GGAACGGTGC
   AAATCACTTG GCAGTCTAGC GGACCTCTGC GGTAGGTGGG ACAAACCTGG AGGTATCTTC TGTGCCCCCTG GCTAGGTGCG AGGCGCCGCG CCTTGCCACG

701 ATTGGAACGC GGATTCCCCG TGCCAAGAGT GACGTAAGTA CCGCCTATAG AGTCTATAGG CCCACCCCCCT TGGCTTCGTT AGAACGCGGC TACAATTAA
   TAACCTTGGC CCTAAGGGGC ACGGTTCTCA CTGCATTTCAT GGCGGATATC TCAGATATCC GGGTGGGGGA ACCGAAGCAA TCTTGCGCCG ATGTTAATTA

801 ACATPAACCTT ATGPATCATA CACATACGAT TTAGGTGACA CTATAGAATA ACATCCACTT TGCCTTTCTC TCCACAGGTG TCCACTCCCA GGTCCAAC
   TGTATGGAA TACATAGTAT GTGTATGCTA AATCCACTGT GATATCTTAT TGTAGGTGAA ACGGAAAGAG AGGTGTCCAC AGGTGAGGCT CCAGGTTGAC

901 CACCTCGGTT CTATCGATTG AATTCCACCA TGGGATGGTC ATGTATCATC CTTTTTCTAG TAGCAACTGC AACTGGAGCG TACGCTGAGG TTCAGCTGTT
   GTGGAGCCAA GATAGCTAAC TTAAGGTGGT ACCCTACCG TACATAGTAG GAAAAGATC ATCGTTGACG TTGACCTCGC ATCGGACTCC AAGTCGACCA

1  M G W S C I I L F L V A T A T G A Y A E V Q L V
   ^start signal peptide ^start of heavy chain
   ^met ^BsiWI

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**FIG.\_34A**

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1001 GGAGTCTGGC GGTGGCCTGG TGCAGCCAGG GGGCTCCTC CGTTGTCTCT GTGCAGCTTC TGGCTTCACC ATTAGTGGTT CTGGGATACA CTGGGTGCGT
    CCTCAGACCG CCACCGGACC ACGTCGGTCC CCGGAGTGAG GCAAACAGGA CACGTGGAAG ACCGAAGTGG TAATCACCAA GAACCTATGT GACCCACGCA
25  E S G G G L V Q P G G S L R L S C A A S G F T I S G S W I H W V R
    ^CDR-H1

1101 CAGGCCCCCG GTAAGGGCCT GGAATGGGTT SCTTGGATTG CTCCTTATAG CGGGCTACT GACATATGCC ATAGCGTCAA GGGCCGTTTC ACTATAAGCG
    GTCCGGGGCC CATTCCCGGA CCTTACCCAA CGAACCTAAC GAGGAATATC GCGCGATGA CTGATACGGC TATCGCAGTT CCCGGCAAAG TGATATTCCG
58  Q A P G K G L E W V A W I A P Y S G A T D Y A D S V K G R F T I S A
    ^CDR-H2

1201 CAGACACATC CAAAACACA GCCTACCTAC AAATGAACAG CTTAAGAGCT GAGGACACTG CCGTCTATTA TTCTGCAAGA GAGGGGGGCT TGTA CTGGST
    GTCTGTGTAG GTTTTGTGT CCGATGGATG TTTACTTGTG GAATCTCGA CTCCTGTGAC GGCAGATAAT AACACGTTCT CTCCCCCGCA ACATGACCCA
92  D T S K N T A Y L Q M N S L R A E D T A V Y Y C A R E G G L Y W V
    ^CDR-H3

1301 GTTCGACTAC TGGGTCAAG GAACCCCTGGT CACCGTCTCC TCGGCTTCCA CCAAGGGCCC ATCGTCTTC CCCTGGCAC CCTCTCCAA GAGCACCTCT
    CAAGTGATG ACCCCAGTTC CTTGGGACCA GTGGCAGAGG AGCCGGAGGT GGTTCCTGGG TAGCCAGAAG GGGGACCGTG GGAGGAGGTT CTCGTGGAGA
125 F D Y W G Q G T L V T V S S A S T K G P S V F P L A P S S K S T S
    ^Apa1

1401 GGGGGCACAG CGGCCCTGGG CTGCCCTGGT AAGGACTACT TCCCCGACC GGTGACGGTG TCGTGGAACT CAGGCGCCCT GACCAGCGGC GTGCACACCT
    CCCCCGTGTC GCGGGGACCC GACGGACCCAG TTCCTGATGA AGGGGCTTGG CCACCTGCCAC AGCACCCTGA GTCCGCGGGA CTGGTCGCCG CACGTGTGGA
158 G G T A A L G C L V K D Y F P E P V T V S W N S G A L T S G V H T F

1501 TCCCGGCTGT CCTACAGTCC TCAGGACTCT ACTCCCTCAG CAGCGTGGTG ACTGTGCCCT CTAGCAGCTT GGGCACCCAG ACCTACATCT GCAACGTGAA
    AGGCCCGACA GGATGTCAGG AGTCTGAGA TGAGGGAGTC GTCGCACCCAC TGACACGGGA GATCGTCGAA CCGTGGGTC TGGATGTAGA CGTTGCACCT
192 P A V L Q S S G L Y S L S S V V T V P S S S L G T Q T Y I C N V N

1601 TCACAAGCCC AGCAACACCA AGGTGGACAA GAAAGTTGAG CCCAAATCTT GTGACAAAC TCACACATGC CCACCGTGCC CAGCACCTGA ACTCCTGGGG
    AGTGTTCCGG TCGTTGTGGT TCCACCTGTT CTTTCAACTC GGGTTTAAAC CACTGTATTG AGTGTGTACG GGTGGCACGG GTCGTGGACT TGAGGACCCC
225 H K P S N T K V D K K V E P K S C D K T H T C P P C P A P E L L G

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**FIG.\_34B**

1701 GGACCGTCAG TCCTCTCTT CCCCCAAA CCAAGGACA CCTCATGAT CTCCCGGACC CCTGAGTCA CATCGTGGT GTGGACGTG AGCCACGAAG  
 CCTGGCAGTC AGAAGAGAA GGGGGGTTTT GGGTTCTGT GGGAGTACTA GAGGCGCTGG GGACTCCAGT GTACGCACCA CCACCTGCAC TCGGTGCTTC  
 258 G P S V F L F P P K P K D T L M I S R T P E V T C V V V D V S H E D  
  
 1801 ACCCTGAGGT CAAGTTCAAC TGGTACGTGG ACGGCGTGG GGTGCATAT GCCAAGACAA AGCCGCGGGA GGACAGTAC AACAGCACGT ACCGGTGGT  
 TGGGACTCCA GTTCAAGTTG ACCATGCACC TGCCGCACCT CCACGTATTA CGGTTCTGTT TCGGCGCCTT CTTGTCATG TTGTCGTGCA TGGCCCCACCA  
 292 P E V K F N W Y V D G V E V H N A K T K P R E E Q Y N S T Y R V V  
  
 1901 CAGCGTCCTC ACCGTCCTGC ACCAGGACTG GCTGAATGGC AAGGAGTACA AGTGCAAGGT CTCCAACAAA GCCCTCCCAG CCCCCATCGA GAAAACCATC  
 GTCCGAGGAG TGGCAGGACG TGGTCTCTGAC CGACTTACCG TTCCTCATGT TCACGTTCCA GAGGTGTTTT CGGAGGGTC GGGGGTAGCT CTTTTGGTAG  
 325 S V L T V L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I  
  
 2001 TCCAAAGCCA AAGGCGAGCC CCGAGAACCA CAGGTGTACA CCTGCCCCC ATCCCGGGAA GAGATGACCA AGAACCAAGGT CAGCCTGACC TGCCTGGTCA  
 AGGTTTCGGT TTCCCGTCGG GGCTCTTGGT GTCCACATGT GGGACGGGG TAGGGCCCTT CTCTACTGGT TCTTGGTCCA GTCCGACTGG ACGGACCAGT  
 358 S K A K G Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C L V K  
  
 2101 AAGGCTTCTA TCCAGCGAC ATCGCCGTGG AGTGGGAGAG CAATGGGCGAG CCGGAGNACA ACTACAAGAC CAGCCTCCC GTCTGGACT CCGACGGCTC  
 TTCCGAAGAT AGGTGCTGTG TAGCGGCACC TCACCTCTC GTTACCCGTC GGCTCTTGT TGATGTTCTG GTGCGGAGG CAGACCTGA GGCTGCCGAG  
 392 G F Y P S D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S  
  
 2201 CTTCCTTCTC TACAGCAAGC TCACCGTGGA CAAGAGCAGG TGGCAGCAGG GGAACGCTTT CTCATGCTCC GTGATGCATG AGGCTCTGCA CAACCACTAC  
 GAAGAAGGAG ATGTCGTTG AGTGGCACCT GTTCTCGTCC ACCGTCGTC CCTTGCAGAA GAGTACGAGG CACTACGTAC TCCGAGACGT GTTGGTGATG  
 425 F F L Y S K L T V D K S R W Q Q G N V F S C S V M H E A L H N H Y  
  
 2301 ACGCAGAGA GCCTCTCCCT GTCTCCGGGT AAATGAGTGC GACGGCCCTA GAGTCGACCT GCAGAAGCTT GCGCGCCATG GCCCAACTG TTTATTGCAG  
 TCGCTCTCT CCGAGAGGGA CAGAGGCCCA TTTACTCAG CTGCCGGAT CTCAGCTGGA CGTCTTCGAA CCGGCGGTAC CCGGTTGAAC AAATAACGTC  
 458 T Q K S L S L S P G K O  
  
 2401 CTTATAATGG TTACAATAA AGCAATAGCA TCACAAATTT CACAAATAA GCATTTTTTT CACTGCATTC TAGTTGTGGT TTGTCCAAC TCATCAATGT  
 GAATATTACC AATGTTTATT TCGTTATCGT AGTGTTTTAA GTGTTTATTT CGTAAAAAA GTGACGTAAG ATCAACACCA AACAGGTTTG AGTAGTTACA

**FIG.\_34C**

2501 ATCTTATCAT GTCTGGATCG ATCGGGAATT AATTGGGGCG AGCACCATGG CCTGAAATAA CCTCTGAAAG AGGAACCTGG TTAGGTACCT TCTGAGGGCG  
TAGAATAGTA CAGACCTAGC TAGCCCTTAA TTAAGCCGGG TCGTGGTACC GGACTTTATT GGAGACTTTC TCCTTGAACC AATCCATGGA AGACTCCGCC

2601 AAACAACCAT CTGTGGAATG TGTGTCAGTT AGGTGTCGGA AAGTCCCCAG GCTCCCCAGC AGCAGAAAGT ATGCAAAAGCA TGCATCTCAA TTAGTCAGCA  
TTTCTTTGGTA GACACCTTAC ACACAGTCAA TCCCACACCT TTCAGGGGTC CGAGGGGTCTG TCCGTCTTCA TACGTTTCGT ACGTAGAGTT AATCAGTCGT

2701 ACCAGGTGTG GAAAGTCCCC AGGTCCCCA GCAGGCAGAA GTATGCAAAG CATGCATCTC AATTAGTCAG CAACCATAGT CCCGCCCTA ACTCCGCCCA  
TGGTCCACAC CTTTCAGGG TCCGAGGGT CGTCCGTCTT CATACGTTTC GTACGTAGAG TTAATCAGTC GTTGGTATCA GGGCGGGGAT TGAGGCGGGT

2801 TCCCGCCCCCT AACTCCGCC AGTTCGCCCC ATTCCTCGCC CCATGGTGA CTAATTTTTT TTATTATTGC AGAGGCCGAG GCCGCCTCG CCTCTGAGCT  
AGGCGGGGA TTGAGGCGG TCAAGGCGG TAAGAGCGG GGTACCGACT GATTAAAAA AATAAATACG TCTCCGGCTC CGGCGGAGCC GGAGACTCGA

2901 ATTCCAGAAG TAGTGAGGAG GCTTTTTTGG AGGCCTAGGC TTTTGCAGAA AGCTGTAAAC AGCTTGGCAC TGGCCGTCGT TTTACAACGT CGTGACTGGG  
TAAGGTCTTC ATCACTCCTC CGAAAAAAC TCCGGATCCG AAAACGTTTT TCGACAATTG TCGAACCGTG ACCGGCAGCA AATGTTGCA GCACTGACCC

3001 AAAACCCCTG CATTACCCAA CTTAATCGCC TTGCAGCACA TCCCCCTTC GCCAGTTGC GTAATAGCGA AGAGGCCCGC ACCGATCGCC CTTCCCAACA  
TTTTTGGGACC GCAATGGGTT GAATTAGCG AACGTCGTGT AGGGGGGAG CGGTCAACCG CATATCGCT TCTCCGGGCG TGGCTAGCGG GAAGGTTGT

3101 GTTGGGTAGC CTGAATGGCG AATGGCGCCT GATGGGGTAT TTTCTCCTTA CGCATCTGTG CGGTATTTC AACCGCATAC GTCAAAGCAA CCATAGTACG  
CAACGCATCG GACTTACCGC TTACCGCGGA CTACGCCATA AAAGAGGAAT GCGTAGACAC GCCATAAAGT GTGGCGTATG CAGTTTCGTT GGTATCATGC

3201 CGCCTGTAG CGGCGCATTA AGCGCGGCG GTGTGGTGGT TACGCGCAGC GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCCGCTCCTT TCGCTTTCTT  
GCGGACATC GCGCGTAAT TCGCGCCGCC CACACCACA ATGCGCCTCG CACTGCGGAT GTGAACGGTC GCGGGATCG GGGCGAGGAA AGCGAAAGAA

3301 CCCTTCCTTT CTCGCCACGT TCGCCGGCTT TCCCCGTCAA GCTCTAATC GGGGGTCCC TTTAGGGTTC CGATTATAGT CTTTACGGCA CCTCGACCCC  
GGGAAGGAAA GAGCGGTGCA AGCGGCCGAA AGGGGCAGTT CGAGATTAG CCCCCAGGG AATCCCAAG GCTAATCAC GAAATGCCGT GGAGCTGGGG

3401 AAAAAACTTG ATTTGGGTGA TGGTTCACGT AGTGGGCCAT CGCCCTGATA GACGGTTTTT CGCCTTTGA CGTTGGAGTC CACGTTCTTT AATAGTGGAC  
TTTTTTTGAAC TAAACCCACT ACCAAGTGCA TCACCCGGTA GCGGGACTAT CTGCCAAAAA GCGGAAACT GCAACCTCAG GTGCAAGAAA TTATCACCTG

FIG.\_34D

3501 TCTTGTTCCTCA AACTGGAACA AACTCAACC CTATCTCGGG CTATCTCTTTT GATTATATAAG GGATTTTGCC GATTTGCGCC TATTGGTTAA AAAATGAGCT  
 AGAACACAGGT TTGACCTTGT TGTGAGTTGG GATAGAGCCC GATAAGAAAA CTAAATATTC CTAAACCGG CTAAACCGG ATAAACCAATT TTTTACTCGA  
  
 3601 GATTTTAACAA AAATTTAACG CGAATTTTAA CAAAATATTA AGTTTACAA TTTTATGGTG CACTCTCAGT ACAATCTGCT CTGATGCCGC ATAGTTAAGC  
 CTAAATTCGT TTTAAATGTC GCTTAAATTT GCTTATAAT TGCAAATGTT AAATATCCAC GTGAGAGTCA TGTTAGACGA GACTACGGCG TATCAATTCG  
  
 3701 CAACCTCCGCT ATCGCTACGT GACTGGGTCA TGGTGGGCC CCGACACCCG CCAACACCCG CTGACGGGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC  
 GTTGAGGGCA TAGCGATGCA CTGACCCAGT ACCGACGGG GGTGTGGG GGTGTGGG GACTGCGGG GACTGCGCGA ACAGACGAGG GCGTAGGGG  
  
 3801 TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT CAGAGGTTTT CACCGTCATC ACCGAAACGC GCGAGGCAGT ATTCTTGAAG ACGAAAGGGC  
 AATGCTCTGTT CGACACTGGC AGAGGCCCTC GACGTACACA GTCTCCAAA GTGGCAGTAG TGGCTTTGCG CGCTCCGTCA TAAGAACTTC TGCCTTCCCG  
  
 3901 CTCGTGATAC GCCTATTTTT ATAGGTTAAT GTCATGATAA TAATGGTTTC TTAGACGTCA GGTGGCACTT TTCGGGGAAA TGTGGCGGA ACCCTATTTT  
 GAGCACATG CGGATAAAAA TATCCAATTA CAGTACTATT ATTACCAAAG AATCTGCAGT CCACCGTGAA AAGCCCTTTT ACACGGCCTT TGGGGATAAA  
  
 4001 GTTTATTTTT CTAAATACAT TCAATATATGT ATCCGCTCAT GAGACAATAA CCCTGATAAA TGTCTCAATA ATATTGAAA AGGAAGAGTA TGAGTATTCA  
 CAAATAAAA GATTATATGTA AGTTTATACA TAGCGGAGTA CTCTGTTATT GGGACTATTT ACGAAGTTAT TATAACTTTT TCCTTCTCAT ACTCATAAAT  
  
 4101 ACATTTCCGT GTCGCCCTTA TTCCCTTTTT TGCGGCATTT TGCCTTCCTG TTTTGTCTCA CCCAGAAACG CTGGTGAAG TAAAGATGC TGAAGATCAG  
 TGTAAAGGCA CAGCGGGAAT AAGGAAAAA ACGCCGTAAA ACGGAAGGAC AAAACGAGT GGGTCTTTGC GACCACTTTC ATTTTCTAGC ACTTCTAGTC  
  
 4201 TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCCGCCCG AAGAAGCTTT TCCAATGATG AGCACTTTTA  
 AACCCACGCG CTCACCCAAT GTAGCTTGAC CTAGAGTTGT CGCATTTCTA GGAACCTCA AAGCGGGGC TTCTTGCAA AGGTTACTAC TCGTGAANAAT  
  
 4301 AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTGATGACCG CGGGCAAGAG CAACTCGGTC GCGGATATCA CTATTTCTCAG AATGACTTGG TTGAGTACTC  
 TTCAAGACGA TACACCCGCG CATATATAGG CACTACTGG GCTTCTCTC GCTGAGCCAG CGCGTATGT GATAAGAGTC TTACTGAACC AACTCATGAG  
  
 4401 ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT GCAGTGCTGC CATAACCATG AGTGATAACA CTGGGCGCAA CTTACTTCTG  
 TGGTCAGTGT CTTTTCGPAG AATGCCCTACC GTACTGTCTAT TCTCTTAATA CGTCACGACG GTATTGGTAC TCACATATGT GACGCGGTT GAATGAAGAC  
  
 4501 ACAACGATCG GAGGACCGAA GGAGCTAACCC GCTTTTTTTC ACAACATGGG GGATCATGTA ACTCGCCCTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA  
 TGTGTCTAGC CTCCTGGGTT CCTCGATTGG CGAAAAACG TGTGTATCCC CCTAGTACAT TGAGCGGAAC TAGCAACCTT TGGCCTCGAC TTAAGTCTGGT

**FIG.\_34E**



4601 TACCAACGA CGAGCGTGAC ACCACGATGC CAGCAGCAAT GGCAACACAG TTGGCGAAAC TATTAACTGG CGACTACTT ACTCTAGCTT CCCGGCAACA  
ATGGTTTGCT GCTCGCACTG TGGTGCTAGG GTCGTCGTGA CCGTTGTTGC AACGCGTTTG ATAATTGACC GCTTGATGAA TGAGATCGAA GGGCCGTTGT

4701 ATTAAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA CTTCTGCGGT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCCGGTGAG  
TAATTATCTG ACCTACCTCC GCCTATTTC ACGTCTCTGGT GAAGACGCCA GCCGGGAAGG CCGACCGACC AAATAACGAC TATTTAGACC TCGGCCACTC

4801 CGTGGGTCTC GCGGTATCAT TGCAGCACTG GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC  
GCACCCAGAG CGCCATAGTA ACGTCGTGAC CCCGGTCTAC CATTCGGGAG GGCATAGCAT CAATAGATGT GCTCCCCCTC AGTCCGTTGA TACCTACTTG

4901 GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA CTGTACAGAC AAGTTTACTC ATATATACTT TAGATTGATT TAAACTTCA  
CTTTATCTGT CTAGCGACTC TATCCACGGA GTGACTAATT CGTAACCAAT GACAGTCTGG TTCAAATGAG TATATATGAA ATCTAACTAA ATTTTGAAGT

5001 TTTTAAATTT AAAAGGATCT AGGTGAAGAT CCTTTTGTAT AATCTCATGA CCAAAATCCC TTATCGTTCC ACTGAGCGTC AGACCCCGTA  
AAAAATTAAA TTTTCTCTAGA TCCACTTCTA GGAATACTA TTAGAGTACT GGTTTTAGGG AATTGCATC AAAAGCAAGG TGACTCGCAG TCTGGGGCAT

5101 GAAAAGATCA AAGGATCTTCT TTTTCTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAC CACCGCTACC AGCGGTGGTT TGTTCGCCG  
CTTTTCTAGT TTCTCTAGAAG AACTCTAGGA AAAAAAGACG CGCATTAGAC GACGAACGTT TGTTTTTTGT GTGCGGATGG TCGCCACCAG ACAAAACGGC

5201 ATCAAGAGCT ACCAATCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG CAGATACCAA ATACTGTCTT TCTAGTGTAG CCGTAGTTAG GCCACCACIT  
TAGTTCTCGA TGGTTGAGAA AAAGGCTTCC ATGACCCGAA GTCGTCTCCG GTCTATGGTT TATGACAGGA AGATCACATC GGCATCAATC CCGTGGTGAA

5301 CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG GTTGACTCA  
GTTCTTGAGA CATCGTGGC GATGTATGGA GCGAGACGAT TAGGACAATG GTCACCGACG ACGGTACCG CTATTCAGCA CAGAATGGCC CAACCTGAGT

5401 AGACGATAGT TACCGGATAA GGGCAGCGG TCGGGCTGAA CGGGGGTTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCCGAA CTGAGATACC  
TCTGCTATCA ATGGCTATT CCGGCTCGCC AGCCCGACTT GCGCCCAAG CACGTGTCTC GGETCGAACC TCGCTGTCTG GATGTGGCTT GACTCTATGG

5501 TACAGCGTGA GCATTGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGG GACAGGTATC CGGTACCGG CAGGTCTGGA ACAGGAGAGC GCACGAGGGA  
ATGTCCGACT CGTAACTCTT TCGCGGTGCG AAGGGCTTCC CTCTTTCCGC CTGTCCATAG GCCATTCGCC GTCCAGCCT TGTCCTCTCG CGTGCTCCCT

5601 GCTTCCAGGG GGAAGCCCT GGTATCTTTA TAGTCTCTGCT GGGTTTCGCC ACCTCTGACT TGAGCGTCTGA TTTTGTGTAT GCTGCTCAGG GGGCGGGAGC  
CGAAGTCCC CCTTTGCGGA CCATAGAAAT ATCAGGACAG CCCAAGCGG TGGAGACTGA ACTCGAGCT AAAAACAATA CGAGCAGTCC CCCCCTCTCG

**FIG. \_34F**

5701 CTATGGAAA ACGCCAGCAA CGCGGCCCTTT TTACGGTTCC TGGCCTTTTG CTGGCCCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCTT GATTCTGTGG  
GATACCTTTT TCGCGTTCGT GCGCCGGAAA AATGCCAAGG ACCGGAAC GACCGGAAA CGAGTGTACA AGAAGGACG CAATAGGGA CTAAGACACC

5801 ATAACCGTAT TACCGCCTTT GAGTGAGCTG ATACCGCTCG CCGCAGCCGA ACGACCAGC GCAGCGAGTC AGTGAGCGAG GAAGCGGAAG AGCGCCCAAT  
TATTGGCATA ATGGCGAAA CTCACTCGAC TATGGCGAGC GCGTCTGGCT TGCTGGCTCG CGTCGCTCAG TCACTCGCTC CTTCGCCCTTC TCGCGGGTTA

5901 ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCAATTA TCCAACCTGG ACGACAGGTT TCCCGACTGG AAAGCGGGA GTGAGCGCAA CGCAATTAAT  
TGCGTTTGGC GGAGAGGGGC GCGCAACCG CTAAGTAATT AGTTGACCG TGCTGTCCAA AGGCTGACC TTTCGCCCGT CACTCGCGTT GCGTAAATTA

6001 GTGAGTTACC TCACTCATTG GGCACCCCG GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA  
CACTCAATGG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA AATACGAAG CCGAGCATAC AACACACCTT AACACTCGCC TATTGTTAAA GTGTGTCTCTT

6101 ACAGCTATGA CCATGATTAC GAATTA  
TGTCGATACT GGTAATAATG CTTAAT

**FIG.\_34G**

LC Frequency											
28	S	N	V	D	G	I	T	L	X		
	511	262	258	186	178	44	39	16	35		
29	I	S	V	G	N	X					
	612	272	254	192	147	70					
30	S	N	K	G	R	Y	T	D	A	X	
	849	176	169	86	81	63	29	28	17	45	
31	S	N	T	R	I	D	K	G	X		
	676	496	170	47	29	28	25	18	53		
32	Y	N	W	F	S	D	R	X			
	1055	128	97	77	61	40	25	69			
50	G	A	D	W	K	L	E	S	X		
	386	341	294	151	116	91	39	30	82		
53	S	N	T	K	I	R	X				
	545	438	407	41	23	23	58				
91	Y	S	R	A	G	H	X				
	849	196	169	118	61	41	148				
92	Y	G	N	S	D	L	T	H	I	X	
	362	356	248	193	114	94	64	43	38	91	
93	S	N	Q	T	H	G	D	R	X		
	738	346	117	101	66	51	47	35	112		
94	S	T	W	Y	L	F	A	P	V	I	
	386	365	288	172	114	79	46	43	33	24	
96	L	Y	W	F	I	R	P	X		N	
	264	205	176	140	117	115	46	121		18	
											X
											40

FIG. 35

Residue	Natural Diversity	Diversity < DNA codon	% good	% covering
L1-28	SNVDGI	SNVDGI<RDT>	100%	94%
L1-29	ISVGN	ISVG<RKT>	100%	86%
L1-29		IV<RTT>	100%	56%
L1-30	SNKGRYTDA	SNKGGRTTDAAE<RVW>	92%	93%
L1-31	SNTRIDKG	SNTTRDKGGAAE<RVW>	75%	95%
L1-31		SNTTRIHK<ANW>	100%	94%
L1-32	YNWFSDR	YNFSDATIV<DHT>	55%	88%
L1-32		YFS<THT>	100%	77%
L2-50	GADWKLES	GAWLSV<KBG>	83%	67%
L2-53	SNTKIR	SNT<AVC>	100%	90%
L3-91	YSRAGH	YSAD<KMT>	75%	74%
		YS<TMT>	100%	66%
L3-92	YGNSDLTHI	YNSDTIFAV<DHT>	67%	64%
		YNSDTA<DMC>	83%	62%
L3-93	SNQTHGDR	SNTGDA<RVT>	83%	80%
		SNTDYAFIV<DHT>	44%	76%
L3-94	STWYLFAPVI	STYLFAPVINDH<NHT>	75%	78%
		STYFIN<WHT>	83%	43%
L3-96	LYWFIRP	LYFPHS<YHT>	67%	52%
		LYFIHN<HWT>	67%	58%
		LFI<HTT>	100%	42%
		LLWR<YKG>	100%	47%
		YF<TWT>	100%	29%

**FIG. 36**

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**Light Chain Designed Diversity**  
Diversity:  $\sim 2.9 \times 10^9$

**CDR-L1: diversity  $\sim 7 \times 10^3$**

28	29	30	31	32
RDT	RTT	RVW	RVW	DHT
D	I	D	D	A
G	V	E	E	D
I		G	G	F
N		K	K	I
S		N	N	N
V		S	S	S
		T	T	T
		R	R	V
				Y

**CDR-L2: diversity = 18**

50	53
KBG	AVC
A	N
G	S
L	T
S	
V	
W	

**CDR-L3: diversity  $\sim 2.3 \times 10^4$**

91	92	93	94	96
KMT	DHT	DHT	NHT	YHT
A	A	A	A	F
D	D	D	D	H
S	F	F	F	L
Y	I	I	H	P
	N	N	I	S
	S	S	L	Y
	T	T	N	
	V	V	P	
	Y	Y	S	
			T	
			V	
			Y	

**FIG. 37**

**Light Chain Designed Diversity**  
Diversity:  $\sim 6.1 \times 10^8$

**CDR-L1: diversity  $\sim 3.4 \times 10^3$**

28	29	30	31	32
RDT	RTT	RVW	ANW	THT
D	I	D	I	F
G	V	E	K	S
I		G	N	Y
N		K	R	
S		N	S	
V		S	T	
		T		
		V		

**CDR-L2: diversity = 18**

50	53
KBG	AVC
A	N
G	S
L	T
S	
V	
W	

**CDR-L3: diversity  $\sim 1.0 \times 10^4$**

91	92	93	94	96
KMT	DMC	RVT	NHT	YHT
A	A	A	A	F
D	D	D	D	H
S	N	G	F	L
Y	S	N	H	P
	T	S	I	S
	Y	T	L	Y
			N	
			P	
			S	
			T	
			V	
			Y	

**FIG. 38**

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**Light Chain Designed Diversity****CDR-L3: diversity  $\sim 1.3 \times 10^3$** 

91	92	93	94	96
TMT	DMC	RVT	WHT	HTT
S	A	A	F	F
Y	D	D	I	I
	N	G	N	L
	S	N	S	
	T	S	T	
	Y	T	Y	

**FIG. 39****CDR-L1**

28	29	30	31	32
RDT	RTT	RVW	RVW	DHT
D	I	D	D	A
G	V	E	E	D
I		G	G	F
N		K	K	I
S		N	N	N
V		S	S	S
		T	T	T
		V	V	V
				Y

**CDR-L2**

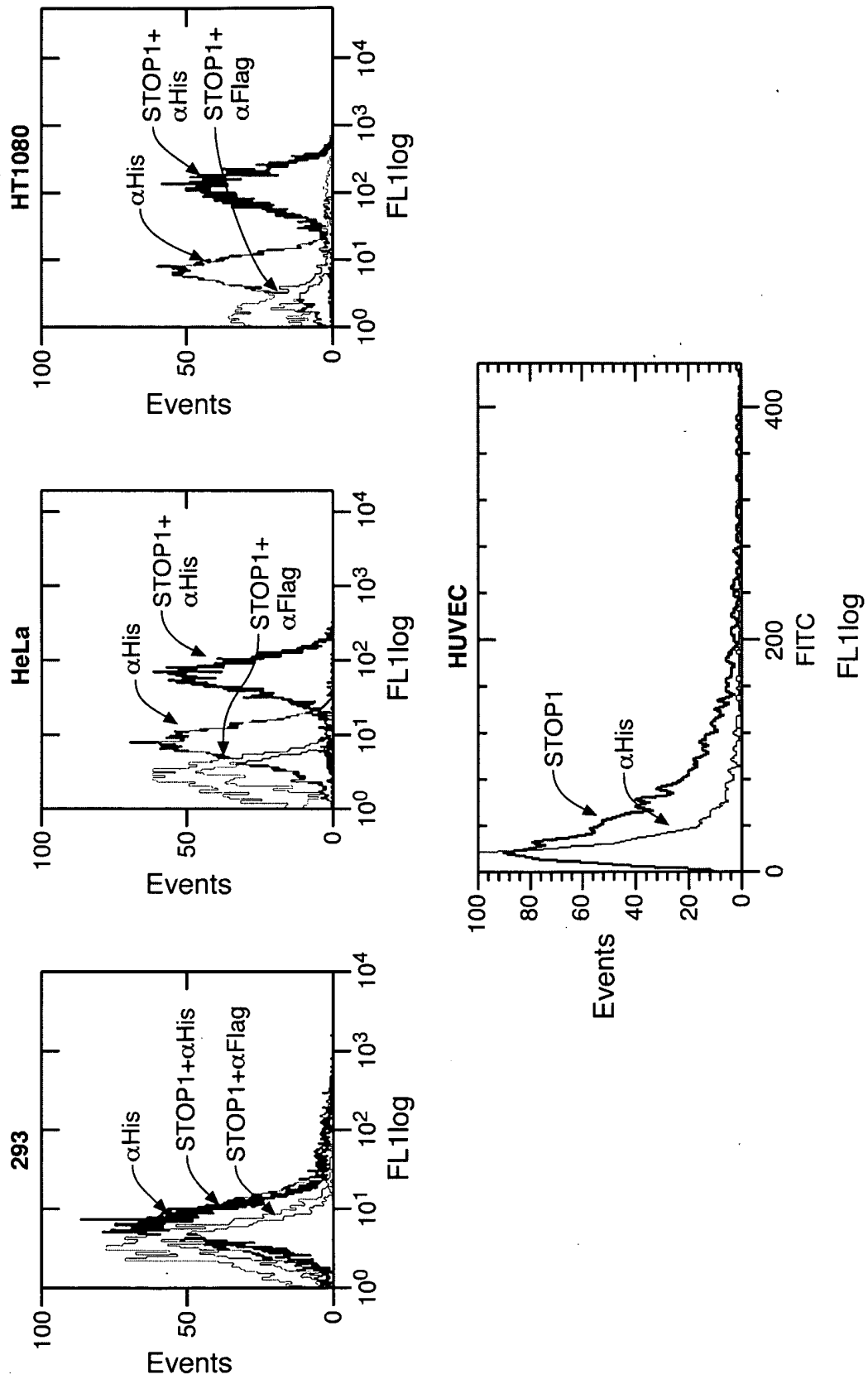
50	53
DVK	AVM
A	N
G	K
L	R
S	S
V	T2
W	

**CDR-L3**

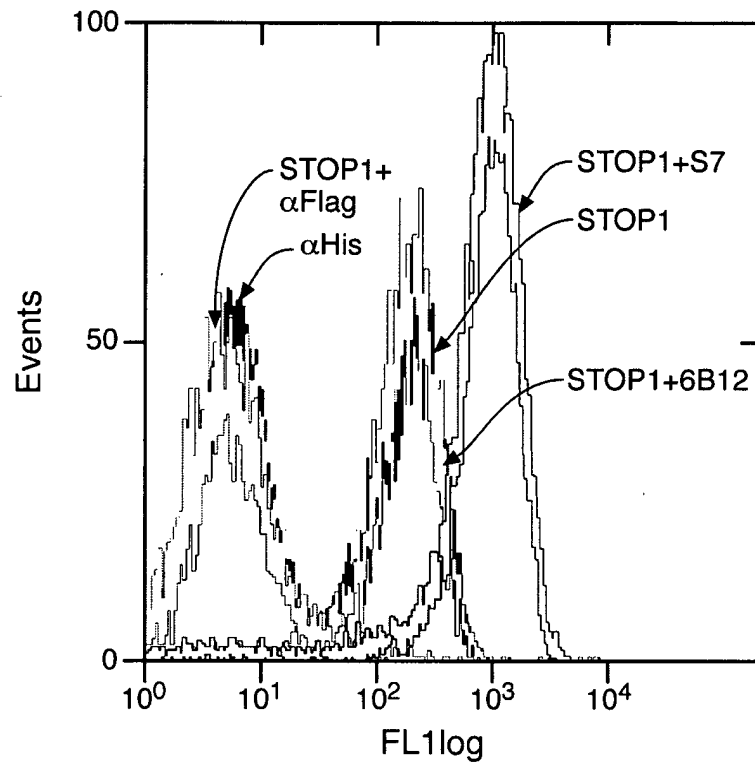
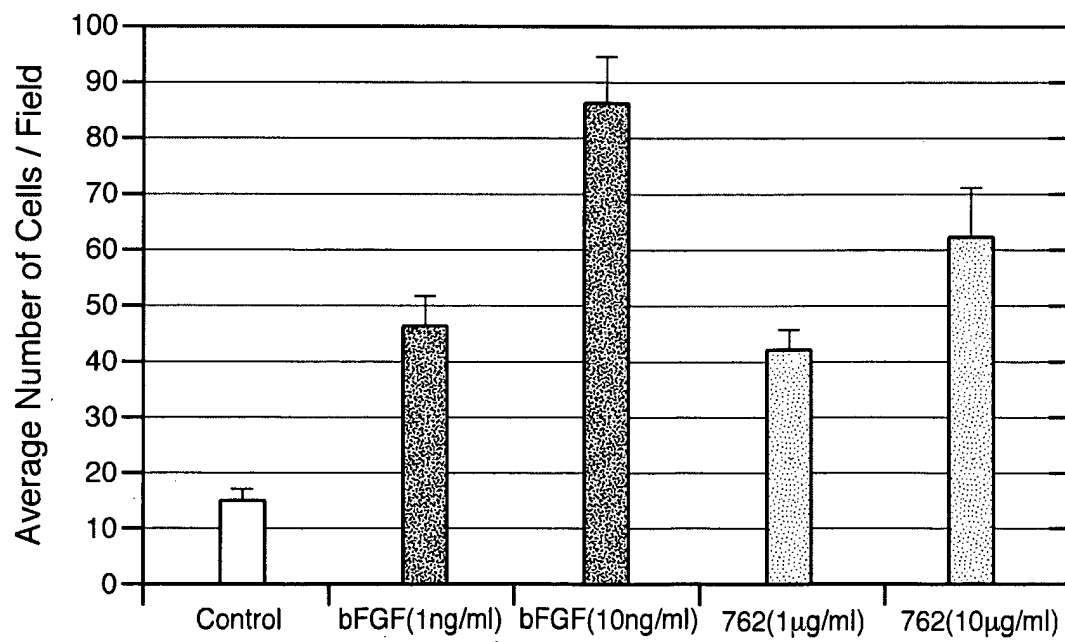
91	92	93	94	96
NRT	NRT	RVM	NNK	TDK
C	C	A2	A	C
D	D	D	C	F
G	G	E	D	L
H	H	G2	E	W
N	N	K	F	Y
R	R	N	G	*
S	S	R	H	
Y	Y	S	I	
		T2	L	
			M	
			N	
			P	
			Q	
			R	
			etc	
			*	

\*Amber stop codon is encoded by the degenerate codon

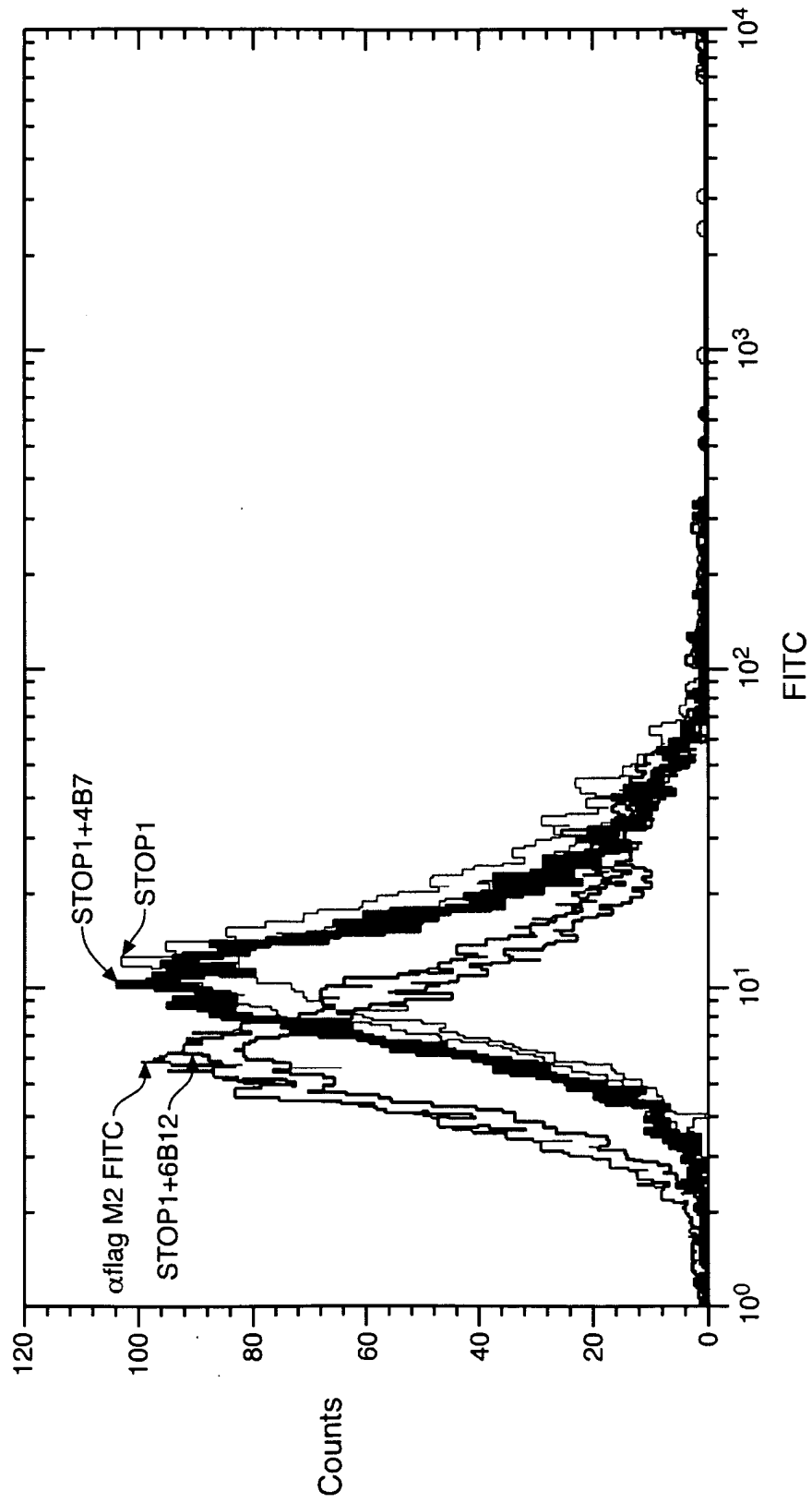
**FIG. 40**

**FIG. 41**

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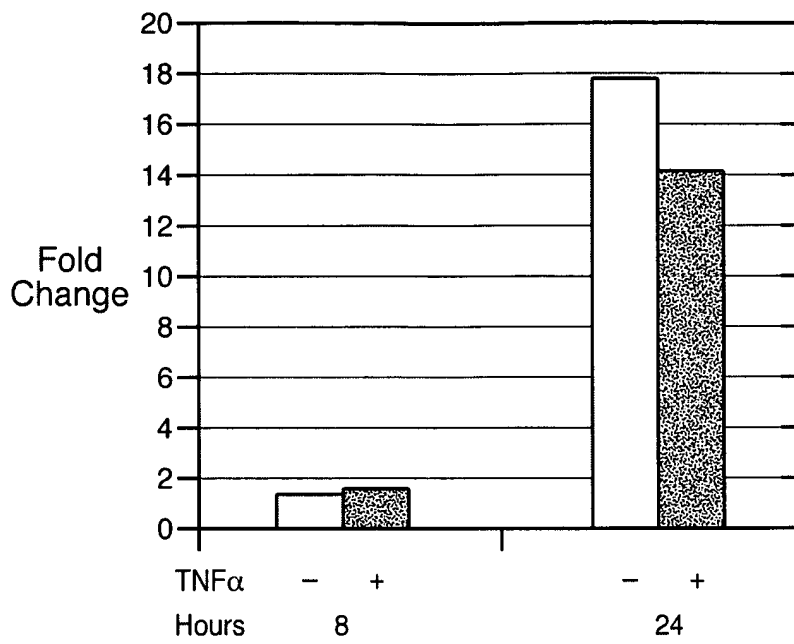
**FIG. 42****FIG. 43**



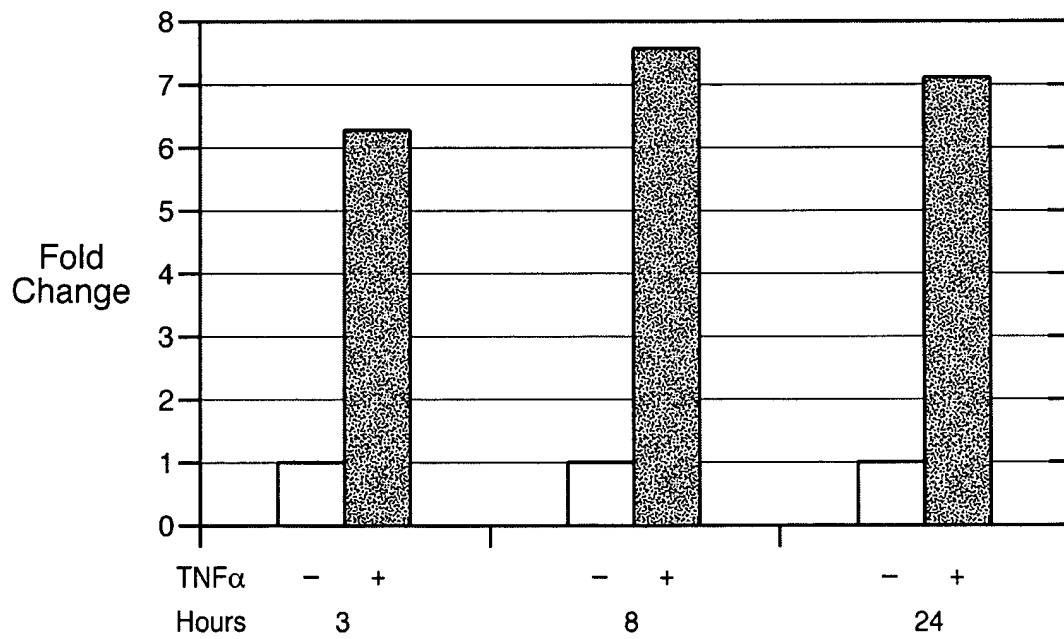
**FIG. 44**

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**FIG. 45A**



**FIG. 45B**